



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 149976**

**TO: Emily M Le**  
**Location: 3c35/3c18**  
**Art Unit: 1648**  
**Wednesday, April 06, 2005**

**Case Serial Number: 10/674666**

**From: Noble Jarrell**  
**Location: Biotech-Chem Library**  
**Rem 1B71**  
**Phone: 272-2556**

**Noble.jarrell@uspto.gov**

### **Search Notes**

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crfe

149976

**Jarrell, Noble**

**From:** Le, Emily  
**Sent:** Tuesday, April 05, 2005 4:38 PM  
**To:** Jarrell, Noble  
**Subject:** Sequence Search: 10/674666

Noble,

Please provide a search for the following:

1. SEQ ID NO: 1

Thanks!

Emily Le  
Office, Rem 3C35  
Mailbox, Rem 3C18  
Tel., 2-0903

Noble

fr 4/6/05

1 AA; Compugen

5 prep; 5 out

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:03 ; Search time 1681 Seconds  
(without alignments)  
80.777 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVFDKNGIHVSEIGEL.....LGMNARCMPLSKRDYKW 409

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	100.0	409	16	US-10-674-666-1 Sequence 1, Appli
2	2116	99.8	409	16	US-10-674-666-2 Sequence 2, Appli
3	2112	99.6	409	16	US-10-674-666-3 Sequence 3, Appli
4	2108	99.4	409	16	US-10-674-666-4 Sequence 4, Appli
5	1797.5	84.8	409	16	US-10-674-666-7 Sequence 7, Appli
6	1793.5	84.6	409	16	US-10-674-666-9 Sequence 9, Appli
7	1793.5	84.6	409	16	US-10-674-666-10 Sequence 10, Appli
8	1789.5	84.4	409	16	US-10-674-666-8 Sequence 8, Appli
9	1764.5	83.2	410	16	US-10-674-666-5 Sequence 5, Appli
10	1763.5	83.2	410	15	US-10-343-175-10 Sequence 10, Appli
11	1760.5	83.0	410	15	US-10-674-666-6 Sequence 6, Appli
12	707.5	33.4	410	15	US-10-369-493-16696 Sequence 16696, A
13	681.5	32.1	413	16	US-10-674-666-19 Sequence 19, Appli

14	679	32.0	411	16	US-10-674-666-13 Sequence 13, Appli
15	670.5	31.6	408	16	US-10-674-666-20 Sequence 20, Appli
16	655	30.9	413	16	US-10-674-666-18 Sequence 18, Appli
17	651.5	30.7	409	16	US-10-674-666-14 Sequence 14, Appli
18	651.5	30.7	409	17	US-10-472-928-4502 Sequence 4502, Ap
19	631.5	29.8	410	15	US-10-369-493-18511 Sequence 21, Appli
20	625	29.5	409	16	US-10-674-666-21 Sequence 21, Appli
21	612.5	28.9	410	16	US-10-674-666-15 Sequence 15, Appli
22	600.5	28.3	409	16	US-10-674-666-16 Sequence 16, Appli
23	532	25.1	403	15	US-10-369-493-8351 Sequence 8351, Ap
24	519	24.5	406	14	US-10-238-075-715 Sequence 715, Ap
25	514	24.2	409	15	US-10-156-761-9857 Sequence 9857, Ap
26	486.5	22.9	418	15	US-10-369-493-13732 Sequence 13732, A
27	476	22.5	399	15	US-10-369-493-7149 Sequence 7149, Ap
28	476	22.5	399	15	US-10-369-493-4394 Sequence 4394, Ap
29	467	22.0	401	15	US-10-369-493-4661 Sequence 4661, Ap
30	467	22.0	402	15	US-10-369-493-7420 Sequence 7420, Ap
31	457	21.6	412	15	US-10-369-493-12226 Sequence 12226, A
32	220	10.4	415	15	US-10-369-493-11106 Sequence 11106, A
33	154	7.3	81	9	US-09-867-550-164 Sequence 164, App
34	136	6.4	105	15	US-10-424-589-164647 Sequence 164647, App
35	113.5	5.4	1270	14	US-10-032-585-7127 Sequence 7127, Ap
36	113	5.3	743	15	US-10-282-122A-74773 Sequence 74773, A
37	109	5.1	453	15	US-10-282-122A-42589 Sequence 42589, A
38	105	5.0	580	16	US-10-674-666-17 Sequence 17, Appli
39	104.5	4.9	740	15	US-10-282-122A-72237 Sequence 72237, A
40	104.5	4.9	1057	15	US-10-282-122A-70305 Sequence 70305, A
41	104.5	4.9	1057	17	US-10-470-048B-152 Sequence 152, App
42	104	4.9	4688	15	US-10-282-122A-76865 Sequence 76865, A
43	103	4.9	495	17	US-10-494-675-14 Sequence 14, Appli
44	103	4.9	502	15	US-10-282-122A-54571 Sequence 54571, A
45	103	4.9	772	13	US-10-121-032-28 Sequence 28, Appli

#### ALIGNMENTS

RESULT 1  
US-10-674-666-1  
; Sequence 1, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PH08001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominus  
US-10-674-666-1

Query Match 100.0%; Score 2120; DB 16; Length 409;  
Best Local Similarity 100.0%; Pred. No. 3.8e-166;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVFDKNGIHVSEIGELVTVLHVEGRREDYTPARLDLFSALIESDARKENOS	60
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QY	61	FKIKMDGINVVELTDVAETVDASAKAKEEPIETFEETVPVLTANKKAVAFILS	120
DB	61	FKIKMDGINVVELTDVAETVDASAKAKEEPIETFEETVPVLTANKKAVAFILS	120
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DB	121	KPTHEMVEFPMMSGITKVELGVESSENELIVDPMPNLYFRDPPASVGVNGVTTHFMRIYVR	180

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Db 181 RETLFARFVFRNHPKLVKTPMYTTPAMKMPLEGDFVYNNETLVVGSERDTDLITLL 240
QY 241 AKNIKANKEVEFKRIIVAINVPRKTNLMHLDITWLMDDKKKFLYSPFIANDVFKFMDYDLVN 300
; AKNIKANKEVEFKRIIVAINVPRKTNLMHLDITWLMDDKKKFLYSPFIANDVFKFMDYDLVN 300
Db 241 AKNIKANKEVEFKRIIVAINVPRKTNLMHLDITWLMDDKKKFLYSPFIANDVFKFMDYDLVN 300
QY 301 GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
; GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
Db 301 GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
QY 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
; IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
Db 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
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RESULT 2
US-10-674-666-2
; Sequence 2, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-2
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Query Match 99.8%; Score 2116; DB 16; Length 409;
Best Local Similarity 99.8%; Pred. No. 8.8e-186;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSVPDSKENGIVHVSIEGLETVLVHBPGRREIDYITTPARLDELFSALIESHDARKHQ 60
QY 61 FVKIMKDGINVELTDLVAETYDLASAKAKEEFLETLEETVPVLTANKKAVAFILS 120
; FVKIMKDGINVELTDLVAETYDLASAKAKEEFLETLEETVPVLTANKKAVAFILS 120
Db 61 FVKIMKDGINVELTDLVAETYDLASAKAKEEFLETLEETVPVLTANKKAVAFILS 120
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; KPTHMVEFMMSGITKYEELGVESENELIYDPMNLYFTRDPASVANGVTIHFMRIYVR 180
Db 121 KPTHMVEFMMSGITKYEELGVESENELIYDPMNLYFTRDPASVANGVTIHFMRIYVR 180
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Db 181 RETLFARFVFRNHPKLVKTPMYTTPAMKMPLEGDFVYNNETLVVGSERDTDLITLL 240
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; AKNIKANKEVEFKRIIVAINVPRKTNLMHLDITWLMDDKKKFLYSPFIANDVFKFMDYDLVN 300
Db 241 AKNIKANKEVEFKRIIVAINVPRKTNLMHLDITWLMDDKKKFLYSPFIANDVFKFMDYDLVN 300
QY 301 GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
; GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
Db 301 GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
QY 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
; IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
Db 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
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RESULT 3
US-10-674-666-3
; Sequence 3, Application US/10674666
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; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-3
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Query Match 99.6%; Score 2112; DB 16; Length 409;
Best Local Similarity 99.8%; Pred. No. 2e-185;
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVPDSKENGIVHVSIEGLETVLVHBPGRREIDYITTPARLDELFSALIESHDARKHQ 60
; MSVPDSKENGIVHVSIEGLETVLVHBPGRREIDYITTPARLDELFSALIESHDARKHQ 60
Db 1 MSVPDSKENGIVHVSIEGLETVLVHBPGRREIDYITTPARLDELFSALIESHDARKHQ 60
QY 61 FVKIMKDGINVELTDLVAETYDLASAKAKEEFLETLEETVPVLTANKKAVAFILS 120
; FVKIMKDGINVELTDLVAETYDLASAKAKEEFLETLEETVPVLTANKKAVAFILS 120
Db 61 FVKIMKDGINVELTDLVAETYDLASAKAKEEFLETLEETVPVLTANKKAVAFILS 120
QY 121 KPTHMVEFMMSGITKYEELGVESENELIYDPMNLYFTRDPASVANGVTIHFMRIYVR 180
; KPTHMVEFMMSGITKYEELGVESENELIYDPMNLYFTRDPASVANGVTIHFMRIYVR 180
Db 121 KPTHMVEFMMSGITKYEELGVESENELIYDPMNLYFTRDPASVANGVTIHFMRIYVR 180
QY 181 RETLFARFVFRNHPKLVKTPMYTTPAMKMPLEGDFVYNNETLVVGSERDTDLITLL 240
; RETLFARFVFRNHPKLVKTPMYTTPAMKMPLEGDFVYNNETLVVGSERDTDLITLL 240
Db 181 RETLFARFVFRNHPKLVKTPMYTTPAMKMPLEGDFVYNNETLVVGSERDTDLITLL 240
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; GGAEPOPOLNGPLDLDKLASIIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGIV 360
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; IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
Db 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVXK 409
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RESULT 4
US-10-674-666-4
; Sequence 4, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-4
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Query Match 99.4%; Score 2108; DB 16; Length 409;
Best Local Similarity 99.5%; Pred. No. 4.8e-185;
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 1 MSVPDSKFNKGINHYSEIGLETLVLAHVEPGRREIDYITPARLDLPSAIIESHDAKREHQS 60
QY 61 FVKIMKDRGINVELTDLVAETVYDLASKAKEEFLETFLEETVPVLTANKKAVAFLLS 120
Db 61 FVKIMKDRGINVELTDLVAETVYDLASKAKEEFLETFLEETVPVLTANKKAVAFLLS 120
QY 121 KPTHEMVEFMMSGITKYEIVGSENELIYDPMPNLYFTFDPFASVGNVGTTHFMRYIYR 180
Db 121 KPTHEMVEFMMSGITKYEIVGSENELIYDPMPNLYFTFDPFASVGNVGTTHFMRYIYR 180
QY 181 RETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFYNNETLVVGSERTDLDITTL 240
Db 181 RETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFYNNETLVVGSERTDLDITTL 240
QY 241 AKNIKANKVEFEKRIIVAINVPRKTNLMHLDITWLTMLDKNKFLYSPINDVFKFMDYDLN 300
Db 241 AKNIKANKVEFEKRIIVAINVPRKTNLMHLDITWLTMLDKNKFLYSPINDVFKFMDYDLN 300
QY 301 GGAEPQPOLNGLPLDKLASTINKKEPVLIPIGAGATEMEIARETNFGDTNYLAIKPGL 360
Db 301 GGAEPQPOLNGLPLDKLASTINKKEPVLIPIGAGATEMEIARETNFGDTNYLAIKPGL 360
QY 361 IGYDRNEKTNALKAAGITVLPFHGNQSLGGMNARCMSPLSRKDYK 409
Db 361 IGYDRNEKTNALKAAGITVLPFHGNQSLGGMNARCMSPLSRKDYK 409
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## RESULT 5

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US-10-674-666-7
; Sequence 7, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-7
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Query Match 84.8%; Score 1797.5; DB 16; Length 409;  
Best Local Similarity 84.4%; Pred. No. 1.7e-156;  
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

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Db 1 MSVPDSKFNKGINHYSEIGLETLVLAHVEPGRREIDYITPARLDLPSAIIESHDAKREHQS 60
QY 61 FVKIMKDRGINVELTDLVAETVYDLASKAKEEFLETFLEETVPVLTANKKAVAFLLS 120
Db 61 FVKIMKDRGINVELTDLVAETVYDLASKAKEEFLETFLEETVPVLTANKKAVAFLLS 120
QY 121 KPTHEMVEFMMSGITKYEIVGSENELIYDPMPNLYFTFDPFASVGNVGTTHFMRYIYR 179
Db 121 KPTHEMVEFMMSGITKYEIVGSENELIYDPMPNLYFTFDPFASVGNVGTTHFMRYIYR 180
QY 181 RETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFYNNETLVVGSERTDLDITTL 239
Db 181 RETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFYNNETLVVGSERTDLDITTL 240
QY 241 AKNIKANKVEFEKRIIVAINVPRKTNLMHLDITWLTMLDKNKFLYSPINDVFKFMDYDLN 299
Db 241 AKNIKANKVEFEKRIIVAINVPRKTNLMHLDITWLTMLDKNKFLYSPINDVFKFMDYDLN 300
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QY 300 NGGABPOPOLNGLPLDKLASTINKKEPVLIPIGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGABPOPOLNGLPLDKLASTINKKEPVLIPIGAGATEMEIARETNFGDTNYLAIKPGL 360
QY 360 VIGYDRNEKTNALKAAGITVLPFHGNQSLGGMNARCMSPLSRKDYK 408
Db 361 VIGYDRNEKTNALKAAGITVLPFHGNQSLGGMNARCMSPLSRKDYK 409
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## RESULT 6

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US-10-674-666-9
; Sequence 9, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-9
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Query Match 84.6%; Score 1793.5; DB 16; Length 409;  
Best Local Similarity 84.1%; Pred. No. 4.1e-156;  
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

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QY 1 MSVPDSKFNKGINHYSEIGLETLVLAHVEPGRREIDYITPARLDLPSAIIESHDAKREHQS 60
Db 1 MSVPDSKFNKGINHYSEIGLETLVLAHVEPGRREIDYITPARLDLPSAIIESHDAKREHQS 60
QY 61 FVKIMKDRGINVELTDLVAETVYDLASKAKEEFLETFLEETVPVLTANKKAVAFLLS 120
Db 61 FVKIMKDRGINVELTDLVAETVYDLASKAKEEFLETFLEETVPVLTANKKAVAFLLS 120
QY 121 KPTHEMVEFMMSGITKYEIVGSENELIYDPMPNLYFTFDPFASVGNVGTTHFMRYIYR 179
Db 121 KPTHEMVEFMMSGITKYEIVGSENELIYDPMPNLYFTFDPFASVGNVGTTHFMRYIYR 180
QY 181 RETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFYNNETLVVGSERTDLDITTL 239
Db 181 RETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFYNNETLVVGSERTDLDITTL 240
QY 240 IAKNIKANKVEFEKRIIVAINVPRKTNLMHLDITWLTMLDKNKFLYSPINDVFKFMDYDLN 299
Db 241 IAKNIKANKVEFEKRIIVAINVPRKTNLMHLDITWLTMLDKNKFLYSPINDVFKFMDYDLN 300
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Db 301 NGGABPOPOLNGLPLDKLASTINKKEPVLIPIGAGATEMEIARETNFGDTNYLAIKPGL 360
QY 360 VIGYDRNEKTNALKAAGITVLPFHGNQSLGGMNARCMSPLSRKDYK 408
Db 361 VIGYDRNEKTNALKAAGITVLPFHGNQSLGGMNARCMSPLSRKDYK 409
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## RESULT 7

```
US-10-674-666-10
; Sequence 10, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
```

PRIOR APPLICATION NUMBER: US 60/427,497  
 PRIOR FILING DATE: 2002-11-18  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 10  
 LENGTH: 409  
 TYPE: PRT  
 ORGANISM: Mycoplasma arthritidis  
 US-10-674-666-10

Query Match 84.6%; Score 1793.5; DB 16; Length 409;  
 Best Local Similarity 84.1%; Pred. No. 4.1e-156;  
 Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVSEIGELVTVLHVEGRIDYITPARLDLFSALIESHARKHQS 60  
 DB 1 MSVDSKFGNGIHVSEIGELSVLVHVEGRIDYITPARLDLFSALIESHARKHQS 60  
 QY 61 FVKIMKRGINNVVELTDLVAETVYDLASQAKKEFIETFEETVAVLTANKKAVRAFLS 120  
 DB 61 FVALKANDINVEETIDLVAEETDVLASQAKDLIEEFLDESEPVLSAEKVVVRAFLKA 120  
 QY 121 KPT-HEMVEFMMSGITTYELGVSENELIVDPMPNLVFTDPFASVNGVTHHMRIVR 179  
 DB 121 KKTSRKLVLMAGITKYDVGADHDLVDPMNLYFTDPFASVNGVTHHMRIVR 180  
 QY 180 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDTTL 239  
 DB 181 RRTLSRFVFNHPKLVNTPMYDDPAMKLSIEGDFVFINNDTLVGVSERTDLDTTL 240  
 QY 240 LAKNIKANKEVEFKIIVAINVPMKTNLMHLDTWLMKDKFLYSPINDVFKFMDYLV 299  
 DB 241 LAKNLVANKCECFKRIIVAINVPMKTNLMHLDTWLMKDKFLYSPINDVFKFMDYLV 300  
 QY 300 NGAEPOQNLGFLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIRKPL 359  
 DB 301 NGAEPOQVENGFLPEKLIQSIINKEPVLIPIAGBASQMEIERETHFDGTNYLAIRPGV 360  
 QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRDKV 408  
 DB 361 VIGYSRNEKTNALKAAGIKVLPFHGNOLSLGMGNARCMSPLSRDKV 409

RESULT 8  
 US-10-674-666-8  
 Sequence 8, Application US/10674666  
 Publication No. US20040131604A1  
 GENERAL INFORMATION:  
 APPLICANT: Clark, Mike A.  
 TITLE OF INVENTION: Method for Inhibiting Viral Replication in vivo  
 FILE REFERENCE: PH080001-100  
 CURRENT APPLICATION NUMBER: US/10/674,666  
 CURRENT FILING DATE: 2003-09-29  
 PRIOR APPLICATION NUMBER: US 60/427,497  
 PRIOR FILING DATE: 2002-11-18  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 8  
 LENGTH: 409  
 TYPE: PRT  
 ORGANISM: Mycoplasma arthritidis  
 US-10-674-666-8

Query Match 84.4%; Score 1789.5; DB 16; Length 409;  
 Best Local Similarity 83.9%; Pred. No. 9.5e-156;  
 Matches 343; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVSEIGELVTVLHVEGRIDYITPARLDLFSALIESHARKHQS 60  
 DB 1 MSVDSKFGNGIHVSEIGELSVLVHVEGRIDYITPARLDLFSALIESHARKHQS 60  
 QY 61 FVKIMKRGINNVVELTDLVAETVYDLASQAKKEFIETFEETVAVLTANKKAVRAFLS 120  
 DB 61 FVALKANDINVEETIDLVAEETDVLASQAKDLIEEFLDESEPVLSAEKVVVRAFLKA 120

DB 61 FVALKANDINVEETIDLVAEETVYDLASQAKDLIEEFLDESEPVLSAEKVVVRAFLKA 120  
 QY 121 KPT-HEMVEFMMSGITTYELGVSENELIVDPMPNLVFTDPFASVNGVTHHMRIVR 179  
 DB 121 KKTSRKLVLMAGITKYDVGADHDLVDPMNLYFTDPFASVNGVTHHMRIVR 180  
 QY 180 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDTTL 239  
 DB 181 RRTLSRFVFNHPKLVNTPMYDDPAMKLSIEGDFVFINNDTLVGVSERTDLDTTL 240  
 QY 240 LAKNIKANKEVEFKIIVAINVPMKTNLMHLDTWLMKDKFLYSPINDVFKFMDYLV 299  
 DB 241 LAKNLVANKCECFKRIIVAINVPMKTNLMHLDTWLMKDKFLYSPINDVFKFMDYLV 300  
 QY 300 NGAEPOQNLGFLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIRKPL 359  
 DB 301 NGAEPOQVENGFLPEKLIQSIINKEPVLIPIAGBASQMEIERETHFDGTNYLAIRPGV 360  
 QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRDKV 408  
 DB 361 VIGYSRNEKTNALKAAGIKVLPFHGNOLSLGMGNARCMSPLSRDKV 409

RESULT 9  
 US-10-674-666-5  
 Sequence 5, Application US/10674666  
 Publication No. US20040131604A1  
 GENERAL INFORMATION:  
 APPLICANT: Clark, Mike A.  
 TITLE OF INVENTION: Method for Inhibiting Viral Replication in vivo  
 FILE REFERENCE: PH080001-100  
 CURRENT APPLICATION NUMBER: US/10/674,666  
 CURRENT FILING DATE: 2003-09-29  
 PRIOR APPLICATION NUMBER: US 60/427,497  
 PRIOR FILING DATE: 2002-11-18  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 5  
 LENGTH: 410  
 TYPE: PRT  
 ORGANISM: Mycoplasma arginini  
 US-10-674-666-5

Query Match 83.2%; Score 1764.5; DB 16; Length 410;  
 Best Local Similarity 82.0%; Pred. No. 1.9e-153;  
 Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVSEIGELVTVLHVEGRIDYITPARLDLFSALIESHARKHQS 60  
 DB 1 MSVDSKFGNGIHVSEIGELSVLVHVEGRIDYITPARLDLFSALIESHARKHQS 60  
 QY 61 FVKIMKRGINNVVELTDLVAETVYDLASQAKKEFIETFEETVAVLTANKKAVRAFLS 120  
 DB 61 FVALKANDINVEETIDLVAEETVYDLASQAKDLIEEFLDESEPVLSAEKVVVRAFLKA 120  
 QY 121 KPT-HEMVEFMMSGITTYELGVSENELIVDPMPNLVFTDPFASVNGVTHHMRIVR 179  
 DB 121 KKTSRKLVLMAGITKYDVGADHDLVDPMNLYFTDPFASVNGVTHHMRIVR 180  
 QY 180 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDTTL 239  
 DB 181 RRTLSRFVFNHPKLVNTPMYDDPAMKLSIEGDFVFINNDTLVGVSERTDLDTTL 240  
 QY 240 LAKNIKANKEVEFKIIVAINVPMKTNLMHLDTWLMKDKFLYSPINDVFKFMDYLV 299  
 DB 241 LAKNLVANKCECFKRIIVAINVPMKTNLMHLDTWLMKDKFLYSPINDVFKFMDYLV 300  
 QY 300 NGAEPOQNLGFLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIRKPL 359  
 DB 301 NGAEPOQVENGFLPEKLIQSIINKEPVLIPIAGBASQMEIERETHFDGTNYLAIRPGV 360  
 QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRDKV 409  
 DB 361 VIGYSRNEKTNALKAAGIKVLPFHGNOLSLGMGNARCMSPLSRDKV 409



DB 361 VIGSRNEKTNAALEAAGIKVLPFHGNOQLSGMGNARCMSPLSRKDYVM 410

RESULT 10  
US-10-343-175-10  
; Sequence 10, Application US/10343175  
; Publication No. US20040096437A1  
; GENERAL INFORMATION:  
; APPLICANT: AngiLab, Inc.  
; TITLE OF INVENTION: The pharmaceutical composition containing arginine deiminase for  
; TITLE OF INVENTION: Inhibiting angiogenesis  
; FILE REFERENCE: PCA/KR01/01281  
; CURRENT APPLICATION NUMBER: US/10/343,175  
; CURRENT FILING DATE: 2003-01-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Kopatentia 1.71  
; SEQ ID NO 10  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acids coding Mycoplasma Arginine Deiminase  
US-10-343-175-10

Query Match 83.2%; Score 1763.5; DB 15; Length 410;  
Best Local Similarity 82.0%; Pred. No. 2,4e-153;  
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVPDSKENGIVHSEIGLETLVLAHPEGREIDYITPARLDLPSALIESHDARKHQS 60  
DB 1 MSVPDSKENGIVHSEIGLESVLVHPEGREIDYITPARLDLPSALIESHDARKHQS 60  
QY 61 FYKIMKDRGINVELTDVAETDYDASAKAEEFETPLEETVPVLTANKKAVRAFLIS 120  
DB 61 FVAELKANDINVELIDVAETDYDASAKAEEFETPLEETVPVLTANKKAVRAFLIS 120  
QY 121 KPT-HEMVEFMMSGITTKYELGVSESENELVDDPMNLYFTRDPFASVGNQVTHFMRYIR 179  
DB 121 KPTSELVEIMMAGITTKYELGVSESENELVDDPMNLYFTRDPFASVGNQVTHFMRYIR 180  
QY 180 RRETLFARVFNHPEKLVTPMYDYPAMKPIEGGDVFIYNNETLVGVSERTDLDITL 239  
DB 181 QRETLFSRPFVFNHPEKLVTPMYDYPAMKPIEGGDVFIYNNETLVGVSERTDLDITL 240  
QY 240 LAKNIKANKVEPKRIIVAINVPEKMTNMLDITLMDKPKFLYSPDIANDVFKFMDYDLY 299  
DB 241 LAKSIVANKECEPKRIIVAINVPEKMTNMLDITLMDKPKFLYSPDIANDVFKFMDYDLY 300  
QY 300 NGGAEPOPQNLPLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGL 359  
DB 301 NGGAEPOPQNLPLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIRPGV 360  
QY 360 VIGYRNEKTNAALEAAGITVLPFHGNOQLSGMGNARCMSPLSRKDYVM 409  
DB 361 VIGYRNEKTNAALEAAGIKVLPFHGNOQLSGMGNARCMSPLSRKDYVM 410

RESULT 11  
US-10-674-666-6  
; Sequence 6, Application US/10674666  
; Publication No. US20040431604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for inhibiting viral replication in vivo  
; FILE REFERENCE: PHE0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 410

; TYPE: PRT  
; ORGANISM: Mycoplasma arginini  
US-10-674-666-6

Query Match 83.0%; Score 1760.5; DB 16; Length 410;  
Best Local Similarity 81.7%; Pred. No. 4,4e-153;  
Matches 335; Conservative 38; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVPDSKENGIVHSEIGLETLVLAHPEGREIDYITPARLDLPSALIESHDARKHQS 60  
DB 1 MSVPDSKENGIVHSEIGLESVLVHPEGREIDYITPARLDLPSALIESHDARKHQS 60  
QY 61 FYKIMKDRGINVELTDVAETDYDASAKAEEFETPLEETVPVLTANKKAVRAFLIS 120  
DB 61 FVAELKANDINVELIDVAETDYDASAKAEEFETPLEETVPVLTANKKAVRAFLIS 120  
QY 121 KPT-HEMVEFMMSGITTKYELGVSESENELVDDPMNLYFTRDPFASVGNQVTHFMRYIR 179  
DB 121 KPTSELVEIMMAGITTKYELGVSESENELVDDPMNLYFTRDPFASVGNQVTHFMRYIR 180  
QY 180 RRETLFARVFNHPEKLVTPMYDYPAMKPIEGGDVFIYNNETLVGVSERTDLDITL 239  
DB 181 QRETLFSRPFVFNHPEKLVTPMYDYPAMKPIEGGDVFIYNNETLVGVSERTDLDITL 240  
QY 240 LAKNIKANKVEPKRIIVAINVPEKMTNMLDITLMDKPKFLYSPDIANDVFKFMDYDLY 299  
DB 241 LAKNIKANKVEPKRIIVAINVPEKMTNMLDITLMDKPKFLYSPDIANDVFKFMDYDLY 300  
QY 300 NGGAEPOPQNLPLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIKPGL 359  
DB 301 NGGAEPOPQNLPLDKLASIINKEPVLIPIGAGATEMEIARETNPDGTNYLAIRPGV 360  
QY 360 VIGYRNEKTNAALEAAGITVLPFHGNOQLSGMGNARCMSPLSRKDYVM 409  
DB 361 VIGYRNEKTNAALEAAGIKVLPFHGNOQLSGMGNARCMSPLSRKDYVM 410

RESULT 12  
US-10-369-493-16696  
; Sequence 16696, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052) B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 16696  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-369-493-16696

Query Match 33.4%; Score 707.5; DB 15; Length 410;  
Best Local Similarity 40.9%; Pred. No. 3,3e-56;  
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVSEIGLETLVLAHPEGREIDYITPARLDLPSALIESHDARKHQSFKYIMKDRGI 70  
DB 5 IHVSEIGLETLVLAHPEGREIDYITPARLDLPSALIESHDARKHQSFKYIMKDRGI 64  
QY 71 NVELTDVAETDYDASAKAEEFETPLEETVPVLTANKKAVRAFLISKTHMVEFM 130  
DB 65 EVLYLEKLAEEA-LVDDKTLREEFVDRILKEGQADVNAH-QTLKEYLISFSENEILQKI 121



LENGTH: 408  
TYPE: PRF  
ORGANISM: Enterococcus faecalis  
US-10-674-666-20

Query Match 31.6%; Score 670.5; DB 16; Length 408;

Best Local Similarity 37.9%; Pred. No. 8.3e-53;

Matches 156; Conservative 87; Mismatches 146; Indels 23; Gaps 10;

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QY 11 IHVYSEIGLELVVHPGREGIDYITPALDELLEFSAILSHDARKEHOSFYKIMKDRGI 70
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 INVFSBIGLKTVMLEHPPGKELENLMPDYLERLLFDDIPLEKACQAEHDAFAELLRSKDI 64

QY 71 NVVELTDLVAETVYDLASKAKAEPIETPLEETVPVLTANKKAVRAFLLS-KPTHENVEP 129
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 EYVYLEDLAEEA--LTNEEVRRQFIQFLBE-ANIRSESAKEKVERLEMLEIDDNELIQK 121

QY 130 NMSGITKVELG-----VESENELIVDPWPNLYFTRDPFASVNGVTIHFMRVYR 179
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 ATAGIQKQELPKVEQEFLLDMVEADVPFIIDPWPNLVFTRDNPATMGHISLNHMYSVTR 181

QY 180 RRETLFARFVFRNHPKLV--KTPWYDPMKMPISGQVFIYNNETLVVGVSEKIDDTI 237
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 QRETI FGQYIFDYHPRFAGKEVPRVDRSESTRIEGDEILISKEVVAIGISQRTDASI 241

QY 238 TLLAKNIKANKKEVEPRIVAINVPMKWTNLMHLDTWLTMKXKELVSP-IANDVFEKWDY 296
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 EKIAIRNIFEQK-LGFKNILAFDIGEHRKFMHLDVFTMIDYDKFTIHPEIBGGLVVSIT 300

QY 297 DLVNGGAEPQOLNGLPLDKLASIINKEPV-LIPIGAGATEMEIARETNFDGTYLAI 355
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 EKADGDIDQITKED--TLDNILCKYHLNVLIRGAGNLT--AAARQWMDGSNTLAI 356

QY 356 KEGLVIGYDRNEKTNAAALAGITVLPHGNQSLGNGNARCMSMPLSRKDV 407
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 357 APGEVVVYDRNFTITNKALEEAGVKNLYIGSELVGRGGRCSMPLYREDL 408
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Search completed: April 6, 2005, 06:23:14  
Job time : 1683 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:04 ; Search time 18 Seconds  
(without alignments)  
2186.259 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120  
Sequence: 1 MSVFDKFKNGIHVYSEIGEL.....LGMGNARCMSPLSRKDKVKW 409

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1764.5	83.2	410	2 A41465	arginine deiminase
2	1702.5	80.3	410	2 S68515	probable arginine
3	679	32.0	411	2 A38835	streptococcal anti
4	651.5	30.7	409	2 D95251	arginine deiminase
5	640.5	30.2	411	2 C90071	arginine deiminase
6	638	30.1	408	2 AE1437	arginine deiminase
7	632	29.8	410	2 AD1080	arginine deiminase
8	631.5	29.8	410	2 E86879	arginine deiminase
9	625	29.5	409	2 T46741	arginine deiminase
10	612.5	28.9	410	2 H70204	arginine deiminase
11	540	25.5	198	2 S73857	arginine deiminase
12	531	25.0	406	2 AB1060	arginine deiminase
13	502.5	23.7	407	2 F82323	arginine deiminase
14	490	23.1	238	2 S73858	arginine deiminase
15	484	22.8	419	2 C95376	probable arginine
16	471.5	22.2	418	2 S02138	arginine deiminase
17	471	22.2	409	2 G95307	arginine deiminase
18	442.5	20.9	402	2 D70602	probable arginine
19	440.5	20.8	247	2 H98115	arginine deiminase
20	363.5	17.1	438	2 S73608	arginine deiminase
21	196.5	9.3	149	2 A99716	arginine deiminase
22	183	8.6	341	2 H90267	arginine deiminase
23	158.5	7.5	287	2 C83872	hypothetical prote
24	148.5	7.0	293	2 A96946	N-dimethylarginine
25	134.5	6.3	486	2 T44863	arginine deiminase
26	113.5	5.4	263	2 C69856	conserved hypothet
27	110.5	5.2	1157	2 AD1728	ATP-dependent deox
28	109.5	5.2	739	2 S39975	stringent response
29	107	5.0	492	2 T09756	catalase (EC 1.11.

30	107	5.0	575	2 T48579	auxin-regulated pr
31	105.5	5.0	1334	2 T41524	rho1 gdp-gtp excha
32	105	5.0	580	2 T45064	arginine deiminase
33	105	5.0	593	2 T04446	hypothetical prote
34	105	5.0	645	2 F86627	LysR family transac
35	105	5.0	4452	1 YGBSG2	gramicidin S synch
36	104.5	4.9	274	2 T2495	probable N-G-N-G-d
37	104.5	4.9	492	2 T09754	catalase (EC 1.11.
38	104.5	4.9	528	2 F70218	GMP synthase (glut
39	104.5	4.9	1057	2 F89892	carbamoyl-phosphat
40	104	4.9	492	2 G5076	hypothetical prote
41	104	4.9	4688	2 F82885	lanosterol synthas
42	103.5	4.9	749	2 T48782	probable Arg-bindi
43	103.5	4.9	1030	2 S43211	probable amino aci
44	103	4.9	502	2 H81273	carbamoylphosphate
45	103	4.9	1065	2 D97225	

ALIGNMENTS

RESULT 1

A41465  
arginine deiminase (EC 3.5.3.6) - Mycoplasma arginini  
N:Alternate names: arginine dihydrolase; lymphocyte blastogenesis inhibitory factor (LBIF)  
C:Species: Mycoplasma arginini  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: A41465; A60538; S11893  
R:Ohno, T.; Ando, O.; Sugimura, K.; Taniai, M.; Suzuki, M.; Fukuda, S.; Nagase, Y.; Yaman  
Infect. Immun. 58, 3788-3795, 1990  
A:Title: Cloning and nucleotide sequence of the gene encoding arginine deiminase of Mycop  
A:Reference number: A41465; MUID:91034196; PMID:2228248  
A:Accession: A41465  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-410 <OHN>  
A:Cross-references: UNIPROT:P23793; EMBL:X54312; NID:G296370; PID:CAA38210.1; PID:G29637  
A:Note: part of this sequence, including the amino end of the mature protein, was confir  
R:Miyaazaki, K.; Takaku, H.; Umeda, M.; Fujita, T.; Huang, W.; Kimura, T.; Yamashita, J.;  
Cancer Res. 50, 4522-4527, 1990  
A:Title: Potent growth inhibition of human tumor cells in culture by arginine deiminase i  
A:Reference number: A60538; MUID:90315609; PMID:2164440  
A:Accession: A60538  
A:Molecule type: protein  
A:Residues: 2-18,'G' <MIY>  
A:Note: the source was designated as Mycoplasma  
R:Kondo, K.; Sone, H.; Yoshida, H.; Toida, T.; Kanatani, K.; Hong, Y.M.; Nishino, N.; Tar  
Mol. Gen. Genet. 221, 81-86, 1990  
A:Title: Cloning and sequence analysis of the arginine deiminase gene from Mycoplasma arg  
A:Reference number: S11893; MUID:90220524; PMID:2325633  
A:Accession: S11893  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-75,'T',77-119,'S',121-125,'E',127-374,'DKKDYLRPISI' <KON>  
A:Cross-references: EMBL:X52459; NID:948705; PID:CAA36693.2; PID:94691328  
C:Genetics:  
C:Genetic code: SGC3  
C:Function:  
A:Description: catalyzes the hydrolysis of arginine to citrulline and ammonia  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase  
F:2-410/Product: arginine deiminase #status predicted <MAT>

Query Match 83.2%; Score 1764.5; DB 2; Length 410;  
Best Local Similarity 82.0%; Pred. No. 1.9e-117;  
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;  
Qy 1 MSVFDKFKNGIHVYSEIGELTVLVHPEGRIDYITPARLDELLFSAILESARKEHQ 60  
Db 1 MSVFDKFKNGIHVYSEIGELTVLVHPEGRIDYITPARLDELLFSAILESARKEHQ 60  
Qy 61 FVKIMKRGGINVVELTDLVAETYLASKAAKEETETFEETVPVLTEANKVAFALLS 120

Db 61 FVAELKANDINVELIDVIAETSYDLASQAKDLIEBFELESEBPVLSEEHKVVVNFLLKA 120  
Qy 121 KPT-HEMVFPWMSGITKYELGVESNELIVDPMNLYFTRDPFASVGVNGVTIHFMRVIVR 179  
Db 121 KKTSRKLVIEIMAGITKYDLGLIEADHELIVDPMNLYFTRDPFASVGVNGVTIHFMRVIVR 180  
Qy 180 RRETLPFARFVRNHPKLVKTPWYDPAKMPDIEGGDVFYNNETLVVGVSERTDLDITL 239  
Db 181 QRETLFSRFSVSNHPKLVNTWYDPSLKSIEGGDVFYNNETLVVGVSERTDLDITL 240  
Qy 240 LAKNIKANKVEFKRIVAINVVKWNTLMHLDITLMTLDKKNFLYSPDIANDVFKFWDYDLV 299  
Db 241 LAKNIVANKECFKRIIVAINVVKWNTLMHLDITLMTLDKKNFLYSPDIANDVFKFWDYDLV 300  
Qy 300 NGGAEPQPOLNGLPLDKLLASIIINKEPVLPIPIGGAGATEMEIARETNFGDTNYLAIKPGL 359  
Db 301 NGGAEPQPVENGPLEGLLQSIINKKPVLIPIAGGASQMEIERETHFDTNYLAIRPGV 360  
Qy 360 VIGYDRNEKTNAALKAAGITVLPFHGNQSLGCMGNARCMSPLSRKDVVKW 409  
Db 361 VIGYSRNEKTNAALKAAGIKVLPFHGNQSLGCMGNARCMSPLSRKDVVKW 410

RESULT 2

S68515  
probable arginine deiminase (EC 3.5.3.6) - Mycoplasma arginini (fragment)  
C:Species: Mycoplasma arginini  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 07-Dec-1999  
R:Wilm, M.; Shevchenko, A.; Houthaeve, T.; Breit, S.; Schweigerer, L.; Fotsis, T.; Mann, Nature 379, 466-469, 1996  
A:Title: Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray  
A:Reference number: S68514; MUID:96158883; PMID:8559255  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-410 <KIL>  
A:Cross-references: EMBL:X93471  
A:Note: only a part of the translation is shown  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995  
A:Accession: S68514  
A:Molecule type: protein  
A:Residues: 103-105,'X',107-111;126,'XX',129-134,'X',136-137;161-167,'D',169-171,'X',173  
A:Note: peptides obtained by mass spectrometry  
C:Genetics:  
C:Genetic code: SGC3  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase

Query Match 80.3%; Score 1702.5; DB 2; Length 410;  
Best Local Similarity 78.3%; Pred. No. 4.6e-113;  
Matches 321; Conservative 48; Mismatches 40; Indels 1; Gaps 1;  
Qy 1 MSVFSKFNIGIHYVSEIGLETLVLPVHPEGRIDYITPARDELLEFSAILEDHARKEHOS 60  
Db 1 MSVFSKFNIGIHYVSEIGLETLVLPVHPEGRIDYITPARDELLEFSAILEDHARKEHOS 60  
Qy 61 FVKIMKDRGINVELDITVAETDLASKAKEEFIELEETVPLTEANKKAVRAFLLS 120  
Db 61 FVEILKQGINVELDITVAETDLASKAKEEFIELEETVPLTEANKKAVRAFLLS 120  
Qy 121 -KPTHEMVFPWMSGITKYELGVESNELIVDPMNLYFTRDPFASVGVNGVTIHFMRVIVR 179  
Db 121 LKSTKELIQTMMAGITKYDLGLIEADHELIVDPMNLYFTRDPFASVGVNGVTIHFMRVIVR 180  
Qy 180 RRETLPFARFVRNHPKLVKTPWYDPAKMPDIEGGDVFYNNETLVVGVSERTDLDITL 239  
Db 181 QRETLFSKFIPTNHPKLVKTPWYDPAKMPDIEGGDVFYNNETLVVGVSERTDLDITL 240  
Qy 240 LAKNIKANKVEFKRIVAINVVKWNTLMHLDITLMTLDKKNFLYSPDIANDVFKFWDYDLV 299  
Db 241 LAKNIKANKVEFKRIVAINVVKWNTLMHLDITLMTLDKKNFLYSPDIANDVFKFWDYDLV 300

Qy 300 NGGAEPQPOLNGLPLDKLLASIIINKEPVLPIPIGGAGATEMEIARETNFGDTNYLAIKPGL 359  
Db 301 NGGSNPEPVVNGLPDLKLLSIIINKKPVLIPIAGKATIEPAVETHFDGTNYLAIKPGV 360  
Qy 360 VIGYDRNEKTNAALKAAGITVLPFHGNQSLGCMGNARCMSPLSRKDVVKW 409  
Db 361 VIGYSRNVKTNAALKAAGIKVLPFHGNQSLGCMGNARCMSPLSRKDVVKW 410  
RESULT 3  
A38835  
streptococcal antitumor protein - Streptococcus pyogenes  
C:Species: Streptococcus pyogenes  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A38835; S16694  
R:Kanaoka, M.; Kawanaka, C.; Negoro, T.; Fukita, Y.; Taya, K.; Agui, H. Agric. Biol. Chem. 51, 2641-2648, 1987  
A:Title: Cloning and expression of the antitumor glycoprotein gene of Streptococcus pyogenes  
A:Reference number: JE0061  
A:Accession: A38835  
A:Molecule type: DNA  
A:Residues: 1-411 <KAN>  
A:Cross-references: UNIPROT:P16962; EMBL:X55659; NID:q47340; PIDN:CAA39192.1; PID:q47341  
R:Kanaoka, M.; Negoro, T.; Kawanaka, C.; Agui, H.; Nabeshima, S. Agric. Biol. Chem. 55, 743-750, 1991  
A:Title: Streptococcal antitumor protein: expression in Escherichia coli cells and proper  
A:Reference number: JH0364; MUID:91234346; PMID:1368629  
A:Accession: A33225  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-57 <KA2>  
C:Superfamily: arginine deiminase arca

Query Match 32.0%; Score 679; DB 2; Length 411;  
Best Local Similarity 39.4%; Pred. No. 1.5e-40;  
Matches 163; Conservative 70; Mismatches 155; Indels 26; Gaps 10;  
Qy 11 IHVYSEIGELETVLVHPEGRIDYITPARDELLEFSAILEDHARKEHOSFVKIMKDRGI 70  
Db 7 IHVYSEIGLKKVLLHHPFGKEIENLMPDYLERLLFDDIPFLEDAQKSHDAPAAQALRDEGI 66  
Qy 71 NVVELTDLVAETDYDLASKAKEEFIELEETVPLTEANKKAVRAFLLS-KPTHEMVFE 129  
Db 67 EVLYLETLAAS--LVTPREARFIDYLS-ANIRGRATKAIKRELLMALEDNQELIEK 123  
Qy 130 MMSGITKYELG-----VSENELIVDPMNLYFTRDPFASVGVNGVTIHFMRVY 177  
Db 124 TMAGVQKSELPEIPASEKGLTDLVESNVYPAIDPMNLYFTRDPFATIGTGVSLNMFSE 183  
Qy 178 VRRRETLFARFVRNHPKL--VKTPWYDPAKMPDIEGGDVFYNNETLVVGVSERTDLD 235  
Db 184 TRNRETLGYKFIYTHPIYGGKVPWYVDRNETTRIEGGDELVLVKDVLAVGISQRTDAA 243  
Qy 236 TITLLAKNIKANKVEFKRIVAINVVKWNTLMHLDITLMTLDKKNFLYSPDIANDVFKFW 294  
Db 244 STEKLLVNI-FKQNLGFKVLAFFANNRKFHMLDTVFTVVDYDKFTIHPHIEGDLRV-- 300  
Qy 295 DYDLVNGGAEPPQOLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMEIARETNFGDTNYL 353  
Db 301 -YSVTYDNEELHIVEEGDLAELLAANLGVKVDLIIRCGDNL--VAAGREQWMDGNSNTL 357  
Qy 354 AIKPGVLVGYDRNEKTNAALKAAGITVLPFHGNQSLGCMGNARCMSPLSRKDV 407  
Db 358 TIAPGVVVVYVNRNTITNAILSKGLKLIKHSSELVGRGPRGRCMSMPFEREDI 411

RESULT 4

D95251  
arginine deiminase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: D95251  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

DESL MODEL SIMILARITY 33.7%, FREQ. NO. 7,36-36,

Db	117	IKKLSMGGVITKPKKHLNEMMDEQYFFFLDPLPNLIYFTRDPAAVTGGSVTINKMPQ	176
Qv	177	IVRRRETILFARFYVRNHPKL--VKTPWYDYPAMKMPIEGGDVFYNNETLIVGVSERTDL	234

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QY 177 I VRRRETLFARFVFRNHPKL--VKTPWYYDPAMKMPIEGGDVFTYNNETLVGVGSERTDL 234
```

Db 177 PARRRESFIELILKHHPFSSQEIPIWSGREPPFPFLEGGDELILNEETVLVGVSERTDA 236  
Qy 235 DTITLLAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKELYSP-IANDVFKF 293  
Db 237 RAVELAESL-FSRAPKIKRVLAASIPETRSMHLDTVFTWVNFQAFTIHPAIONQOQEL 295  
Qy 294 WDYDL--VNGGAPQOLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMEIARETNFDGT 350  
Db 296 NVYILEKSENGLEITPRD---FKRVIARVLGVPEVDPIPCGEDV--IVSAREQWNGDA 350  
Qy 351 NYLAIKPGLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
Db 351 NTLAIAPGEVITYDRNHVSNLLRRKAGIKVHEVISSELSRGRGPRCMTMPITRGNLK 408  
RESULT 7  
AD1080  
arginine deiminase homolog lmo0043 [imported] - Listeria monocytogenes (strain EGD-e)  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AD1080  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karsel, U.  
Science 294, 849-852, 2001  
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1080  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-410 <GLA>  
A:Cross-references: UNIPROT:O8YAS0; GB:NC\_003210; PIDN:CAC98258.1; PID:gl6409402; GSPDB:  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0043  
C:Superfamily: arginine deiminase arca  
Query Match 29.8%; Score 632; DB 2; Length 410;  
Best Local Similarity 37.5%; Pred. No. 3.2e-37;  
Matches 156; Conservative 78; Mismatches 152; Indels 30; Gaps 11;  
Qy 11 IHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKORGI 70  
Db 7 LNIITSEIGKQIVLVKRPFGSELENITPEYLESLLFDDIPYLKMKQKEHDFFAKTWRDSNI 66  
Qy 71 NVVELTDLVAETYDLASAKAEEFIETPLEETVPVLTEANKKA--VRAFLLSKPTHEMVE 128  
Db 67 EVLYLEKLAABALREANN--KESFLTKMIKES---NQMDSEALYVRDYLMSFDEEEMIR 120  
Qy 129 FMSGITKYELGVSENEL-----IVDPMENLYFTDRDPASVGVNGYTIHFMRIV 178  
Db 121 KMGSLKASEIPERKKGHLNEMDQYFFLDPLNLYFTDRDPAVINGVNGYTIHRMFQPA 180  
Qy 179 RRRETLFARFVRNHPKLK--TPWYDPAKMPFIEGGDVFYNNETLVVGVSERTDLD 236  
Db 181 RRRESIFELILKHHPSPNQDIPWSGRGPFPFSLGGDELVLNEETVLVGVSERTDARA 240  
Qy 237 ITLLAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKELYSP-IANDVFKFWD 295  
Db 241 VERLAESL-FNRSPKIKRVLAASIPETRSMHLDTVFTWVNFQAFTIHPAIONQOQELNI 299  
Qy 296 YDL--VNGGAPQOLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMEIARETNFDGTNY 352  
Db 300 YILEKSENGLEITPRD---FORVIAEVLDEPEDIPIPCGEDV--IVSAREQWNGDANT 354  
Qy 353 LAIKPGLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
Db 355 LAIAPGEVITYDRNQVSNLLRSAGIKVHEVISSELSRGRGPRCMTMPVLVRENLK 410  
RESULT 8

EB6879  
arginine deiminase (EC 3.5.3.6) [imported] - Lactococcus lactis subsp. lactis (strain IL1  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: EB6879  
R:Boilotin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp  
A:Reference number: AB6625; MUID:21235186; PMID:11337471  
A:Accession: EB6879  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-410 <STO>  
A:Cross-references: UNIPROT:P58013; GB:AE005176; PID:gl2725086; PIDN:AAK06135.1; GSPDB:GB  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arca  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase  
Query Match 29.8%; Score 631.5; DB 2; Length 410;  
Best Local Similarity 37.3%; Pred. No. 3.4e-37;  
Matches 156; Conservative 70; Mismatches 163; Indels 29; Gaps 6;  
Qy 9 NGIHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDR 68  
Db 3 NGINVNSEIGKLSVLLHRPGAEVENITPDTMKQLLFDIPYLKIAQKEHDFFAQTLRDN 62  
Qy 69 GINVELTDLVAETYDLASAKAEEFIETPLEE-----TVPVLTEANKKAVRAFLLSK 121  
Db 63 GAETVYIENLATEVFEKSSE-TKEEFLSHLLHEAGYRPGRTYDGLTE-----YLTSM 113  
Qy 122 PTHEMVFMSGITKYEL-----GVESNELIVDPMNLYETROPFASVGVNGVT 170  
Db 114 STKDMVEKIYAGVRKNELDIKRTALSMDAGSDAENYFLNPLFNAYFTRDPOQASMGVGM 173  
Qy 171 IHPMRYIVRRRETLFARFVRNHPKLKVTWYDPAKMPFIEGGDVFYNNETLVVGVSE 230  
Db 174 INKMTFAPRQPESLITEYVMANHPFKDTPIWDRNHTTRIEGGDELILNKTTVAIGVSE 233  
Qy 231 RTDLDTITLLAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKELYSP-IANDV 290  
Db 234 RTSKKTIONLAKELFANPLSTFDTVLAVEIPHNNHAMHLDTVFTMINHDQFTVPFGIMDG 293  
Qy 291 FKFWDYDLVNGGAPQOLNGL-PLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDG 349  
Db 294 AGNINVLIPRGKDDVEIEHLTDLKAALKKVLNLSLDLIECAG-DPIAAPREQWNDG 352  
Qy 350 TNYLAIKPGLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407  
Db 353 SNTLAIAPGEIVTYDRNVYTVVELLKEHGIVKHEITLSELGRGRGRCMQSOPLWREDL 410  
RESULT 9  
T46741  
arginine deiminase (EC 3.5.3.6) [validated] - Lactobacillus sakei  
C:Species: Lactobacillus sakei  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T46741  
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C  
J. Bacteriol. 180, 4154-4159, 1998  
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of t  
A:Reference number: Z23141; MUID:98361904; PMID:9696763  
A:Accession: T46741  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-409 <ZUN>  
A:Cross-references: UNIPROT:O53088; EMBL:AJ001330; NID:g2764610; PIDN:CAA04682.1; PID:g2:  
C:Genetics:  
A:Gene: arca  
C:Function:  
A:Description: EC 3.5.3.6 [validated, MUID:98361904]  
A:Pathway: arginine catabolism



C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase

Query Match 29.5%; Score 625; DB 2; Length 409;  
Best Local Similarity 37.4%; Pred. No. 9.8e-37;  
Matches 153; Conservative 77; Mismatches 159; Indels 20; Gaps 8;

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QY 11 IHVYSEIGETLVVHFGREIDYITPARLDELLSAILSHDARKEHQSFKVIMKDRGI 70
DB 5 IHVNSEIGKLVLLKRPGEVENITPDIMYRLFFDDIPYLPYIQKEHDDQFAQTURDNGV 64
QY 71 NVVELTDLVAETDYLASKAAKEFEETETLEETVTVPLTEANKKAVRAFLLSKPTHEMVFEM 130
DB 65 EVLYLENLAEAIDAGD--VKBAFLDKMLNES-HIKSPQVQALKYDLISWATLDMVSKI 121
QY 131 MSGITKYLGVES-----ENELIVDPNPNLYTRDPPFASVGVNGVTIHFMYIIVRR 180
DB 122 MAGVRTNEIDIKSKALIDVADDDYDFYMDPMPNLYTRDPAASMGDLTKINTMFEARQ 181
QY 181 RETLFARFVRNHPKLVK--TPWYYDPAMKMPLEGDDVFYNNETLVVGVSBERTDLDTIT 238
DB 182 RESMFEMVIMQHPRAFGQAQVWRDRDHIDRMGGDELLISDKVLAIGISQRTSAQSIE 241
QY 239 LLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFVLSPIANDVFKFWD-YD 297
DB 242 ELAKVLFANHS-GFSEKILAIKIPHKHAMMHLDTVFTMIDYDKFTTHPGIQGAGGMVDYI 300
QY 298 LVNGGAEPQQLNGPLDKLLASIIIN-KEPVLIPIGGAGATEMEIARETDFGTNYLAIK 356
DB 301 LEPGNNDKIKITHQTDLEKVLRLDALEVPETLIPCGGDA--VVAPEQWNGDSNTLAIA 358
QY 357 POLVIGYDRNEKTNAAKAGITVLPFGNQLSLGNGNARCMSPLSRK 405
DB 359 PGVVVYDRNYVSNENLRQYGIKVIEVSPSELSRGGPRCMSGMLPLVR 407
```

## RESULT 10

H70204  
arginine deiminase (arca) homolog - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: H70204  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A:Reference number: A70100; MUID:98065943; PMID:9403685  
A:Accession: H70204  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-410 <KLE>  
A:Cross-references: UNIPROT:O51781; GB:AE001183; GB:AE000783; NID:g2688786; PIDN:AAC6719  
A:Experimental source: strain B31  
C:Superfamily: arginine deiminase arca

Query Match 28.9%; Score 612.5; DB 2; Length 410;  
Best Local Similarity 36.5%; Pred. No. 7.6e-36;  
Matches 152; Conservative 73; Mismatches 161; Indels 31; Gaps 10;

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QY 9 NGIHVYSIGELETVLVHFGREIDYITPARLDELLSAILSHDARKEHQSFKVIMKDR 68
DB 7 NPINIFSEIGRLKVLKRRPGBELENLPLIMKNFLFDDIPYLVKVRQGEHEVFVNILKDN 66
QY 69 GINVELTDLVAETDYLASKAA-KEEFTETLEEIVTVPLTEANKKAVRAFLLSKPTHEMV 127
DB 67 SVEIETVEDLVSEV--LASSVALKNKFTISQFTILE-AEIKTDGVINILDKYFNSLTFVDMNV 123
QY 128 EFMMSGITKVEL-----GVSENELIVDPMNLYTRDPPFASVGVNGVTIHFMYIIV 178
DB 124 SKMISGVAREELKCOCEFSLDDWNGSSLFVIDPMPNVLFTTRDPPFASVGVNGVTIHFMYIIV 183
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QY 179 RRRETLFARFVRNHPKLVK-TPWYYDPAMKMPLEGDDVFYNNETLVVGVSBERTDLDTI 237
DB 184 RRRETIFAEYIFKYHSAAYKENVPWFNWRWEETSLEGDFVNLNKLDDLVIGISERTAGSV 243
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFVLSPIANDVFKFWDYD 297
DB 244 EKLAASLFPNK-APSTILAFKIPQRAYMHLDTVFTQIDYS--VFTSFTSDDMYFSIYV 300
QY 298 LVNGGAEPQQLNGPLDKLLASIIINKEPVLPIPIG-----AGATEMEIARETDFGT 350
DB 301 LTVNS-----NSNKINIKKEKAKL--KDVLSFYLRKIDIIKACGGDLIHGAREQWNDGA 353
QY 351 NYLAIKPGLVIGYDRNEKTNAAKAGITVLPFGNQLSLGNGNARCMSPLSRKDV 407
DB 354 NVLAIAPEGVIAYSRNVHTNKLFBENGIKVHRIPSELSRGGPRCMSGMLSLVREDI 410
```

## RESULT 11

S73857  
arginine deiminase (EC 3.5.3.6) arca - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein H10\_orf198  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73857  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73857  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-198 <HIM>  
A:Cross-references: EMBL:AE000052; GB:U00089; NID:g1674223; PIDN:AAB96179.1; PID:g167422;  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: arca  
A:Genetic code: SGC3  
C:Keywords: hydrolase

Query Match 25.5%; Score 540; DB 2; Length 198;  
Best Local Similarity 55.3%; Pred. No. 3.8e-31;  
Matches 109; Conservative 30; Mismatches 52; Indels 6; Gaps 2;

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QY 211 IEGGDVFYNNETLVVGVSBERTDLDTITLAKNIKANKEVEFKRIVAINVPKWTNLMHLD 270
DB 4 IEGGDIFVYDQQTVMVGLSERTTEAAINVLAKKIQDSSSTSFGRIFVINVPQLPNLMHLD 63
QY 271 TWLTMLDKNKFVLSPIANDVFKFWDYDLVNGGAPQPOLNGL--PLDKLLASIIINKEPVL 328
DB 64 TWLTMLDRNKFVSPNMLAVLKAWRIDF---TDPALKWNEIAGDLSTILHTIIGQKQPL 119
QY 329 IPIGGAGATEMEIARETDFGTNYLAIKPGLVIGYDRNEKTNAAKAGITVLPFGHQL 388
DB 120 IPIAGADANQETIEIETHFDGTNYLTAPSVVVGARYAKNLTHQTLAAAGVKVIAFKGNQL 179
QY 389 SLGNGNARCMSPLSRK 405
DB 180 SLGNGSARCMSPVLRK 196
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## RESULT 12

AB1060  
arginine deiminase (EC 3.5.3.6) [imported] - Salmonella enterica subsp. enterica serovar  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AB1060  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connorson, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AB1060  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD06927.1; PID:gl6505575; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY4805  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase

Query Match 25.0%; Score 531; DB 2; Length 406;  
Best Local Similarity 32.9%; Pred. No. 4.4e-30;  
Matches 136; Conservative 74; Mismatches 172; Indels 32; Gaps 9;

QY 13 VYSEIGELTVLVAHPGREGIDYITPARLDELFSAILSHDARKEHQSFVKIMKDRGINV 72  
DB 6 VOSEIGQLRSVMHRPNLSKRLTFSNCQELFDVLSVERAGEHDIFANTLROGGIEV 65  
QY 73 VELTDLVAETYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMVFMS 132  
DB 66 LLTDLTLLTQTLVDAD--AKAWLLDTQISDY--RLGPTFAADIRAWLADMPHRELARHLSG 121  
QY 133 GITKVELGVSEB-----NELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVRRRET 183  
DB 122 GUTYGEIPASIKMNVVDTHDINDFMKPLNHLFTRDTSCWITNGVSNPMAKPARQRET 181  
QY 184 LPARFVFRNHPKLVKTPWY-----YDPAMKMPIEGGDVFIYNNETLVVGVSEDTL 234  
DB 182 NNLRAIYRWHPOFADGDFIKYFGDENINYDHA---TLGGDVLVIGRAVLIGMSERTTP 238  
QY 235 DTITLLAKNIKANKVEFEKRIVAIVPKWTNLMLHLDTWLMDKNKF-LYSPINDVFKF 293  
DB 239 QGVFLAQLFKHQAE--RVIAVELPKHRSCHMLDVTWTHIDIDTFSYFVVRPDVQC 296  
QY 294 WYDYLNGVGAEPQPLGLPLDKLLASINKEPVLIPIGGAGATEMEIARETNDGTNYL 353  
DB 297 W--TLTPDGRGLKRTQBSTLVALETALGIDQVRLITTTGGDAFEAE--REQWNDANNVL 352  
QY 354 AIKPLGLVIGYDRNEKTNAAKAAAGITVLPFGNQLSLGMGNARCMSPLSKDV 407  
DB 353 TLRPGVVGYERNITWNEKYDKAGITVLPFGDELGRGRCARCMSCLERDGI 406

RESULT 13  
F82323  
arginine deiminase VC0423 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: F82323  
R:Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H  
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: AB2035; MUID:20406833; PMID:10952301  
A:Accession: F82323  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-407 <HEI>  
A:Cross-references: UNIPROT:O9KUU2; GB:AE004130; GB:AE003852; NID:G9654845; PIDN:AAF9359  
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor  
C:Genetics:  
A:Gene: VC0423  
A:Map position: 1  
C:Superfamily: arginine deiminase arca

Query Match 23.7%; Score 502.5; DB 2; Length 407;  
Best Local Similarity 31.8%; Pred. No. 4.7e-28;  
Matches 134; Conservative 79; Mismatches 171; Indels 37; Gaps 9;

QY 9 NGIHVYSIGELETVLVHVPGRREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDR 68

DB 2 NRLVGVSEVGQLRRVLLNRPERALTHLTPSNCHELLFDDVLAVEAAGVEHDAFANTLRTQ 61  
QY 69 GINVELTDLVAETYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMVE 128  
DB 62 DVELLLHDLLEET--LAIPAROWLLNTQISDRFGPTFA--RELRLHMLNHLDDHLLTT 117  
QY 129 FMMSGITKVELGVSEB-----ELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVR 179  
DB 118 LLLGLAFSELHLESDSMLPKMRQPLDFVIEPLNHLFTRDTSCWYGVGSINPMKPAR 177  
QY 180 RRETLPARFVFRNHPKLVKTPW-----YDPAMKMPIEGGDVFIYNNETLVVGVSE 230  
DB 178 QRETNHLRAIYRWHPIFAQHPIFIHYFGDIDLHYDNA---NIEGGDVLVIGKGAVLIGNSE 234  
QY 231 RTDLDTTLLAKNIKANKVEFEKRIVAIVPKWTNLMLHLDTWLMDKNKLYSPIANDV 290  
DB 235 RTSQGVENLAAL--FKHQASKVIAINLPHKRSCHMLDVTWTHMDVDTFSVTP--EV 289  
QY 291 FKFWDYDLVNGVGAEPQPLGLPLDKLLASINKEPVL----IPGGAGATEMEIARETN 346  
DB 290 MR---KDLPTWRLTPKNGGDMRVEQVPSYLHAIEQALGVDYLKIITTGGNSYEAREQW 346  
QY 347 PDGTNYLAIKPLGLVIGYDRNEKTNAAKAAAGITVLPFGNQLSLGMGNARCMSPLSR 406  
DB 347 NDANNVLTVKPGVVIGYERNVYTNKYDKAGIKVLTIPGNELGRCRGARCMSCLERDG 406  
QY 407 V 407  
DB 407 I 407

RESULT 14  
S73858  
arginine deiminase (EC 3.5.3.6) arca - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein H10\_Orf238  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C>Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73858  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73858  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-238 <HIM>  
A:Cross-references: EMBL:AE000052; GB:U00089; NID:gl674223; PIDN:AAB96180.1; PID:gl67422f  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: arca  
A:Genetic code: SGC3  
C:Keywords: hydrolase

Query Match 23.1%; Score 490; DB 2; Length 238;  
Best Local Similarity 50.3%; Pred. No. 1.7e-27;  
Matches 97; Conservative 43; Mismatches 47; Indels 6; Gaps 3;

QY 7 KFGIHVYSIGELETVLVHVPGRREIDYITPARLDELFSAILSHDARKEHQSFVKIMK 66  
DB 2 KYN-INVHSEIGLQTVLVHTPGNEIRRISPRLLDILLFSAVIEPDTAIOEHOTFCOLLQ 60  
QY 67 DRGINVVELTDLVAETYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFL--SKPT 123  
DB 61 EQNIEVVQLTDLTATTFDKANATAQNFIEQLDQAPKLTPEHRKAKQYLLEQAKST 120  
QY 124 HEMVEFMSGITKVELGVSEB--ENELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVRRR 181  
DB 121 LSMVRSMMGIDKRVAAANTINGDFLVDMPNLYFTRDPFASIGHGINSINRMKYLTRR 180  
QY 182 ETLFARFVFRNHP 194  
|||||

Job time : 21 secs

Db	181	ETLFASFILPTTP	193
RESULT 15			
C95376			
probable arginine deiminase (EC 3.5.3.6) [imported] - Sinorhizobium meliloti (strain 102			
C/Species: Sinorhizobium meliloti			
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004			
C/Accession: C95376			
R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows			
: Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.			
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001			
A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti			
A/Reference number: A95262; MUID:21396509; PMID:11481432			
A/Accession: C95376			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-419 <KUR>			
A/Cross-references: UNIPROT:Q92YG5; GB:AE006469; PIDN:AAK65573.1; PID:gl4524052; GSPDB:G			
A/Experimental source: strain 1021, megaplasmid pSymA			
R/Gallibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,			
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;			
L.; Hyman, R.W.; Jones, T.			
Science 293, 668-672, 2001			
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,			
hebaault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.			
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.			
A/Reference number: A96039; MUID:21368234; PMID:11474104			
A/Contents: annotation			
C/Genetics:			
A/Gene: arcA2			
A/Genome: plasmid			
C/Superfamily: arginine deiminase arca			
C/Keywords: hydrolase			
Query Match 22.8%; Score 484; DB 2; Length 419;			
Best Local Similarity 29.1%; Pred. No. 9.9e-27;			
Matches 130; Conservative 82; Mismatches 170; Indels 64; Gaps 14;			
Qy	1	MSVPDSKFGIHVYSEIGETVLVHEPGREIDYTPARLDLFLSAILSESHDARKEHQS	60
Db	1	MSSKSSTQHTFGVHSEVQLRKVMWCAFGRAHQRLTPNCDDALLFDVWVDNARDHFD	60
Qy	61	FKVIMKDRGINNVVELTDLVAETYDILASKAAKEEFIEETVP-----VLTEANKKAV	114
Db	61	FMTKMRDRGVEVVEWHNLLAQI--VAIPEARKWILD--NQVVPNQVGLLELDE-----I	110
Qy	115	RAFLLSKPTHEMVEFMMSGITKYL-----GVESENELIVDPMENLYFT	158
Db	111	RSYLEGLPDRLAETLIGGLSTHEFPETHGGEMLELRDAAGVA---EYLLPPLPNTLYT	167
Qy	159	RDPPASVGVGTIHPMRVIVRRRETFLARFVRNHPKLV--KTPWYDPAWK--MPTEG	213
Db	168	RDTTCWYGGVTNPLNYPARHEETILATAIYKHPDFGVKNVWVGFTTDDWGLATLEG	227
Qy	214	GDVFTYNNETLVVGVSRERDLDITLLAKNIKANKEVEFKRIVAINVPRKWTNLMHLDTWL	273
Db	228	GDVMEIGKGNVLIGNSERTSRQAIQLAATLFEKGAQ--RVIVAAMPKRAAMHLDTVF	285
Qy	274	TMLDKN-KFLYSPDIANDVFKWDYDLVNGGABQPQLNGLPLDKLLASIN-----K	324
Db	286	TFADRDCVLIYPDIVEIEAF-----SYRFGKPGSLELHKDRGSFVETVRDALGLK	337
Qy	325	EPVLIPIGGAGATEMEIARETNFD-GTNVLAIKPGIVIGYDRNEKTNAAKAGITVLPP	383
Db	338	ENRVVETGG-----NAYVRERTQWDSGANLVCLSPGVVLAYDRNTYNTLLRKAGVEVITI	393
Qy	384	HGNQLSLGNGNARCMSPILSRKDKVKW	409
Db	394	TGAELGRGGGCHWCPIIRDVDY	419

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:03 ; Search time 182 Seconds  
(without alignments)  
1150.771 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVDSKFNHIVSEIGEL.....LGMGNARCMSPLSRKDVKW 409

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2115	99.8	408	1	ARCA_MYCHO	P41141 mycoplasma
2	1763.5	83.2	409	1	ARCA_MYCAR	P23793 mycoplasma
3	1721.5	81.2	409	2	Q9RND4	Q9rnd4 mycoplasma
4	1169.5	55.2	452	2	Q8EVF6	Q8evf6 mycoplasma
5	1103	52.0	408	2	Q7NBF0	Q7nbf0 mycoplasma
6	1057	49.9	404	1	ARCA_MYCPN	P75475 mycoplasma
7	986	46.5	409	2	Q6KI67	Q6ki67 mycoplasma
8	708.5	33.4	410	2	Q6HP29	Q6hp29 bacillus th
9	707.5	33.4	410	2	Q81111	Q81111 bacillus ce
10	705.5	33.3	410	2	Q73E87	Q73e87 bacillus ce
11	688	32.5	403	2	Q8KZ88	Q8kz88 granulicite
12	682.5	32.2	409	2	Q8GG81	Q8gg81 streptococc
13	681.5	32.1	411	2	Q6ZNR4	Q6znr4 bacillus li
14	681.5	32.1	413	1	ARCA_BACLI	Q6znr4 bacillus li
15	681.5	32.1	413	2	Q6SD88	Q6sd88 bacillus li
16	679	32.0	410	1	ARCA_STRPY	P16962 streptococc
17	678.5	32.0	410	2	Q8DWQ2	Q8dwq2 streptococc
18	678.5	32.0	410	2	Q8E2K0	Q8e2k0 streptococc
19	677	31.9	410	1	ARCA_STRP3	Q8k5f0 streptococc
20	672	31.7	411	2	Q6TK74	Q6tk74 streptococc
21	670.5	31.6	408	2	Q93K67	Q93k67 enterococcu
22	660	31.1	413	1	ARCA_CLOPE	Q46254 clostridium
23	655.5	30.9	409	2	Q9KJG1	Q9kjl1 streptococc
24	651.5	30.7	409	1	ARCA_STRPN	Q97na4 streptococc
25	650	30.7	410	2	Q8GND5	Q8gnd5 streptococc
26	648.5	30.6	411	2	Q6GDG7	Q6gdg7 staphylococ
27	644.5	30.4	411	1	ARCA_STAAW	Q8nuk7 staphylococ
28	644.5	30.4	411	2	Q7AS72	Q7as72 staphylococ
29	644.5	30.4	411	2	Q6G639	Q6g639 staphylococ
30	641.5	30.3	411	1	ARCL_STAEP	P8cgg5 staphylococ
31	640.5	30.2	411	1	ARCA_STAAM	P63553 staphylococ

32	640.5	30.2	411	1	ARCA_STAAN	P63554 staphylococ
33	638.5	30.1	410	1	ARCA_LACLC	Q9k576 lactococcus
34	638.5	30.1	410	2	Q9KGV5	Q9kqv5 lactococcus
35	638	30.1	408	1	ARCA_LISIN	Q92fr7 listeria in
36	632	29.8	410	1	ARCA_LISMO	Q8vas0 listeria mo
37	631.5	29.8	410	1	ARCA_LACLA	P58013 lactococcus
38	631	29.8	410	2	Q725C1	Q725cl listeria mo
39	625	29.5	409	1	ARCA_LACSK	O53088 lactobacill
40	624.5	29.5	410	2	Q73QJ2	Q73qj2 treponema d
41	624.5	29.5	468	2	Q8RDD8	Q8rdd8 thermoanaer
42	621.5	29.3	409	2	Q65ZT1	Q65zt1 borrelia ga
43	617.5	29.1	415	2	Q8VW56	Q8vw56 enococcus
44	613	28.9	411	1	ARCL_STAEP	Q8cmw1 staphylococ
45	612.5	28.9	410	1	ARCA_BORBU	O51781 borrelia bu

ALIGNMENTS

RESULT 1

ARCA\_MYCHO STANDARD; PRT; 408 AA.

AC P41141;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).

GN Name=arca;

OS Mycoplasma hominis.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI\_TaxID=2098;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92396053; PubMed=1522817;

RA Harasawa R., Koshimizu K., Kitagawa M., Asada K., Kato I.;

RT "Nucleotide sequence of the arginine deiminase gene of Mycoplasma

RT hominis.";

RL Microbiol. Immunol. 36:661-665(1992).

CC -! CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).

CC -! PATHWAY: Arginine degradation via arginine deiminase; first step.

CC -! SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -! SIMILARITY: Belongs to the arginine deiminase family.

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EMBL: D13314; BAA02571.1; -.

HA MAP: MF\_00242; -; 1.

DR InterPro: IPR003198; Amidino trans.

DR InterPro: IPR003876; Arg\_deimnase.

DR Pfam: PF02274; Amidinotransf; 1.

DR PRINTS: PR01466; ARGDEIMINASE.

DR TIGRFAMs: TIGR01078; arca; 1.

Arginine metabolism; Hydrolase.

FT INIT\_MET 0 0 By similarity.

FT ACT\_SITE 396 396 Amidino-cysteine intermediate (By

FT similarity).

SQ SEQUENCE 408 AA; 46182 MW; 53A1D6373DBBE93 CRC64;

Query Match 99.8%; Score 2115; DB 1; Length 408;

Best Local Similarity 100.0%; Pred. No. 7e-137;

Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVFDSKFNHIVSEIGELTVLHVEPGREIDYITPARDELFSAILSHDARKEHQSF 61

Db 1 SVFDSKFNHIVSEIGELTVLHVEPGREIDYITPARDELFSAILSHDARKEHQSF 60

Qy 62 VKIMKDRGINVVELTDLVAETDYDLASKAAKBEFTFLEETVPLTEANKKAVRAFLSK 121

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Db 122 PTHMVEFMGSGITKYELGVSENELIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRRR 181
Db 121 PTHMVEFMGSGITKYELGVSENELIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRRR 180
Qy 182 ETLFARFVRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILLA 241
Db 181 ETLFARFVRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILLA 240
Qy 242 KNIKANKEVEFKRIVAINVFKWTLNMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLVNG 301
Db 241 KNIKANKEVEFKRIVAINVFKWTLNMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLVNG 300
Qy 302 GAEPQOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFGTNYLAIKPGGLVI 361
Db 301 GAEPQOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFGTNYLAIKPGGLVI 360
Qy 362 GYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409
Db 361 GYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 408

RESULT 2
ARCA MYCAR
ID ARCA MYCAR STANDARD; PRT; 409 AA.
AC P23793;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).
GN Name=arca;
OS Mycoplasma arginini.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2094;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=ATCC 23838;
RX MEDLINE=94361803; PubMed=7765234; DOI=10.1016/0168-1656(94)90050-7;
RA Misawa S., Aoshima M., Takaku H., Matsumoto M., Hayashi H.;
RT "High-level expression of Mycoplasma arginine deiminase in Escherichia
RT coli and its efficient renaturation as an anti-tumor enzyme.";
RL J. Biotechnol. 36:145-155(1994).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91034196; PubMed=2228248;
RA Ohno T., Ando O., Sugimura K., Taniai M., Suzuki M., Fukuda S.,
RA Nagase Y., Yamamoto K., Azuma I.;
RT "Cloning and nucleotide sequence of the gene encoding arginine
RT deiminase of Mycoplasma arginini.";
RL Infect. Immun. 58:3788-3795(1990).
RN [3]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=KM101;
RX MEDLINE=90220524; PubMed=2325633;
RA Kondo K., Sone H., Yoshida H., Toida T., Kanatani K., Hong Y.-M.,
RA Nishino N., Tanaka J.-I.;
RT "Cloning and sequence analysis of the arginine deiminase gene from
RT Mycoplasma arginini.";
RL Mol. Gen. Genet. 221:81-86(1990).
CC -1- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -1- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the arginine deiminase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; X54141; CAA38080.1; --
CC EMBL; X54312; CAA38210.1; --
CC EMBL; X52459; CAA36693.2; --
CC PIR; A41465; A41465.
CC PDB; 1LXY; X-ray; A/B=1-409.
CC HAMAP; MF 00242; -.
CC InterPro; IPR003198; Amidino trans.
CC InterPro; IPR003876; Arg deiminase.
CC Pfam; PF02274; Amidinotransf; 1.
CC PRINTS; PRO1466; ARGDEIMINASE.
CC TIGRFAMs; TIGR01078; arca; 1.
CC 3D-structure; Arginine metabolism; Direct protein sequencing;
CC Hydrolase.
CC KW
CC INIT_MET 0 0 Amidino-cysteine intermediate (By
CC ACT_SITE 397 397 similarity).
CC
CC CONFLICT 75 75 I -> T (in Ref. 3).
CC CONFLICT 119 119 A -> S (in Ref. 3).
CC CONFLICT 125 125 E -> K (in Ref. 2).
CC CONFLICT 374 409 EAAGIKVLPFHGNQSLGNGNARCMSPLSRKDVKW -> D
CC FT KQDYLRPISI (in Ref. 3).
CC FT
CC SQ SEQUENCE 409 AA; 46376 MW; 71EC4E8D7FB69D61 CRC64;

Query Match 83.2%; Score 1763.5; DB 1; Length 409;
Best Local Similarity 82.2%; Pred. No. 9.1e-113;
Matches 336; Conservative 36; Mismatches 36; Indels 1; Gaps 1;

Qy 2 SVFDSKFGKHVYSEIGELETVLVHPGREDIVTTPARLDELLFSAITLSDHDKHQS 61
Db 1 SVFDSKFGKHVYSEIGELETVLVHPGREDIVTTPARLDELLFSAITLSDHDKHQS 60
Qy 62 VKIMKRGINWVELTDLVAETDYDLASAKAEETETFEETVPLTTPANKKAVRAFLSK 121
Db 61 VAEIKANDINVELDLVAETDYDLASQAKDLEEFLEDEPVLSEHKVAVRNFLKAK 120
Qy 122 PT-HEMVEFMGSGITKYELGVSENELIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRR 180
Db 121 KTSRELVEIMMAGITKYDGLGTEADHEHLIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRRQ 180
Qy 181 RETLFASVFRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILL 240
Db 181 RETLFASVFRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILL 240
Qy 241 AKNIKANKEVEFKRIVAINVFKWTLNMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLV 300
Db 241 AKNIKANKEVEFKRIVAINVFKWTLNMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLV 300
Qy 301 GGABPQOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFGTNYLAIKPGGLV 360
Db 301 GGABPQOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFGTNYLAIKPGGLV 360
Qy 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409

RESULT 3
Q9RND4
ID Q9RND4 PRELIMINARY; PRT; 409 AA.
AC Q9RND4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Arginine deiminase.
GN Name=arca;
OS Mycoplasma arthritidis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG6;
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RX MEDLINE=20353471; PubMed=10894746;
RX DOI=10.1128/JB.182.15.4343-4347.2000;
RA Dyvig K., French C.T., Voelker L.L.;
RT "Construction and use of derivatives of transposon Tn4001 that
RT function in Mycoplasma pulmonis and Mycoplasma arthritidis.";
RL J. Bacteriol. 182:4343-4347(2000).
DR EMBL; AF182646; RAD55448.1; -.
DR HSSP; P23793; 1LXY.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR Pfam; PF02274; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
SQ SEQUENCE 409 AA; 46039 MW; 7FEDC7F182BF5C7 CRC64;

Query Match 81.2%; Score 1721.5; DB 2; Length 409;
Best Local Similarity 80.4%; Pred.No.6.9e-110;
Matches 329; Conservative 38; Mismatches 41; Indels 1; Gaps 1;

QY 1 MSVFDKFGNIHYSEIGELETVLVHPEGREIDYITPARLDELLFSAILSHDARKEHQS 60
Db 1 MSVFDKFGNIHYSEIGELETVLVHPEGREIDYITPARLDELLFSAILSHDARKEHKE 60

QY 61 FVKIMKRGINNVVELTDLVAETDYDLASKAAKEEFIEFTLEETVPLTEANKKAVRAFLS 120
Db 61 FVAELKRGINNVVELVDLVETDYDLASKAAKEKLEEFLLDSAPVLSDSHRAAVKKFLQS 120

QY 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASGVNGVTIHFMYIVR 179
Db 121 QRSTLSLEYMTAGTTHKDLKTESLELIVDPMNLYFTRDPFASGVNGVTIHFMYKYR 180

QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 QRETLFSRVFSNHPKLVNTPWYDPAEGLSIEGGDVFIYNNETLVVGVSERTDLDITL 240

QY 240 LAKNTKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPIANDVFKFWDYDLV 299
Db 241 LAKNTKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPIANDVFKFWDYDLV 300

QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFGTYLAIKQGL 359
Db 301 NGGDAPQPVNDGLPLEDLLKSIIIGKKPTLPIAGAGASQIDIERETHFGTYLAVAPGI 360

QY 360 VIGYDRNEKTNAAKAAAGITVLPFGNQSLGCMGNARCMSPLSRKDVK 408
Db 361 VIGYARNEKTNAAEAGITVLPFRGNQSLGCMGNARCMSPLSRKDVK 409

RESULT 4
QY QBEVF6 PRELIMINARY; PRT; 452 AA.
AC QBEVF6;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DE Arginine deiminase.
GN OrderedLocusNames=MYPE6080;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=1246555; DOI=10.1093/nar/gkf667;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004172; BAC44398.1; -.
DR HSSP; P23793; 1LXY.

DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR Pfam; PF02274; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
SQ SEQUENCE 452 AA; 51045 MW; B2SCCDL5165E59F4 CRC64;

Query Match 55.2%; Score 1169.5; DB 2; Length 452;
Best Local Similarity 56.4%; Pred.No.5.8e-72;
Matches 237; Conservative 68; Mismatches 92; Indels 23; Gaps 4;

QY 1 MSVFD--SKFNGIHVYSEIGELETVLVHPEGREIDYITPARDELLFSAILSHDARKH 58
Db 43 MSSIDKNSLGNINVSIEGELKEVLVHTPGDEIRYAPTAPSRLEELLFSAVLKADTAIEEH 102

QY 59 QSFVKIMKRGINNVVELTDLVAETDYDLASKAAKESFIETLEETVPLTEANKKAVRAFL 118
Db 103 KGFVKILQNGIKVILQCLDLVAETDYELCSKEVRNSFIQYLDLALFVLKKEIRPVVVKYL 162

QY 119 LSKPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASGVNGVTIHFMYIVR 178
Db 163 LSFPTVQVVRKMSGLANELNIKQDNPLIIDGMENLYFTRDPFASMGVNGVINCWKYPT 222

QY 179 RRETLPARFVRNHPKLVKTPWYD--PAMKMPIEGGDVFIYNNETLVVGVSERTDLDIT 237
Db 223 RKREVFISRFVFTNPKYKNTPRYFDIVGNNGTIEGGDIFIYNSKTLVIGNSERTINFAAI 282

QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPIANDVFKFWDYD 297
Db 283 ESVAKNIQANKDCTFERIVINVPMPNLMHLDTWLMDYDFLYSPNMNMVKLIWEID 342

QY 298 LVNGGABEPQOLNGLP-----LDKLLASIIINKEPVLPIPGGAGATEMEIARETNFD 348
Db 343 -----LVNPKVFKVEKKGTLSEVLIIIDKKLILPIACKGANQLDIDIEHFD 391

QY 349 GTNYLAIKPLGVIGYDRNEKTNAAKAAAGITVLPFGNQSLGCMGNARCMSPLSRKDVK 408
Db 392 GTNYLTIAAGVVGVERNEKTKQALVEAGIKVLSPFNGSQLSGMGSARCMSPLEIRENLK 451

RESULT 5
QY Q7NBF0 PRELIMINARY; PRT; 408 AA.
AC Q7NBF0;
DT 01-MAR-2004 (TremBLrel. 26, Created)
DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)
DE ArcA (EC 3.5.3.6).
GN ORFNames=MGA.1220;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(low).";
RL Microbiology 149:2307-2316(2003).
DR EMBL; AE016968; AAP56679.1; -.
DR HSSP; P23793; 1LXY.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR Pfam; PF02274; Arg deiminase.
DR PRINTS; PR01466; ARGDEIMINASE.
DR Complete proteome; Hydrolase.
KW
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SQ SEQUENCE 408 AA; 47084 MW; 36EC0BF5A6A8F58A CRC64;
Query Match 52.0%; Score 1103; DB 2; Length 408;
Best Local Similarity 52.2%; Pred. No. 1.9e-67;
Matches 213; Conservative 79; Mismatches 102; Indels 14; Gaps 4;
QY 8 FNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILEDHARKHQSFVKIMKD 67
DB 7 FNRKRVYSEIGKLRKVLVHTGKELDYVTPQRLDELLFSSLLNPKARQEHETFIKLED 66
QY 68 RGINNVVELTDLVAETYLASAKAABEFTETLEETVPVLTTEANKAVRAFLSKPTHE-- 125
DB 67 HDVECVQLSTLTATQTFQAVNSKIQEFTFNRLDECLPVLSEINRLKVYDYLKSLATNPQV 126
QY 126 MYEFMWSGITYKVELGVSENELVDPMENLYFTDRPPASVGVNGVTIHFMRIVVRRETLF 185
DB 127 MIRKMSGILAKEVGIOSEVELADPMENLYFTDRPPASVGVNGVTIHFMRIVVRRETLF 186
QY 186 ARFVFRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSBERTDLDITILLAKNIK 245
DB 187 ADPIFSHPHPEYKNAPKYYSREDKYSIEGGDLFVYDDKTLVIGVSBERTKKAISOAEKLR 246
QY 246 ANKEVEFKRIIVAINVPKWTNLMHLDTWLTMDKXKFLYSPANDVFKWDYDLVNGGAP 305
DB 247 QNDSTFEKIVAINVPKWSNLMHLDTWLTMDYDKFLYSPNMGMVLKIWEIDLH----- 301
QY 306 QP-----QINGLPDLKLASIINKEPVLPIGGAGATEMEIARETNPDGTNYLAIKPGLV 360
DB 302 -PTLIWRELE-SLEGFSMWIGKATLIPVAGEDSTQIEIDVETNFATNPLVLIQPGV 359
QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
DB 360 VGYDRNYKTQALRDAGVKYVISWNGDQLSLGMSARCMSPLYRDPK 407

RESULT 6
ARCA_MYCPN
ID ARCA_MYCPN STANDARD; PRT; 404 AA.
AC P75475; P75474;
DT 16-OCT-2001 (Rel. 40, Created)
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Putative arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase)
DE (AD).
GN Name=arCA; OrderedLocusNames=MEN304; ORFNames=MP531/MP532;
OS Mycoplasma pneumoniae;
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelreich R., Hilbert H., Plegens H., Firkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the arginine deiminase family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to several
CC frameshifts that produce two separate ORFs.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AE000052; AAB96180.1; ALT FRAME.
DR EMBL; AE000052; AAB96179.1; ALT_FRAME.
DR HAMAP; MF 00242; atypical; 1.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PRO1466; ARGDEIMINASE.
KW Arginine metabolism; Complete proteome; Hydrolase;
KW Hypothetical protein.
FT ACT_SITE 394
FT ACT_SITE 394 Amidino-cysteine intermediate (By
FT similarity).
SQ SEQUENCE 404 AA; 45478 MW; 22A99F5437A7E3BE CRC64;
Query Match 49.8%; Score 1057; DB 1; Length 404;
Best Local Similarity 52.0%; Pred. No. 2.6e-64;
Matches 211; Conservative 76; Mismatches 107; Indels 12; Gaps 5;
QY 7 KFGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILEDHARKHQSFVKIMK 66
DB 2 KYN-INVHSEIGQLQTVLHVHTPGNEIRRIISPRLLDLLFSAVIEPDTAIQEHOTFCOLLQ 60
QY 67 DRGINNVVELTDLVAETYLASAKAABEFTETLEETVPVLTTEANKAVRAFL--SKPT 123
DB 61 EONIEVVQLTDLTRATTFDKANATQNOFIETWLDQAEFKLTPEHKYAKQVYLQAKAST 120
QY 124 HEMVFMWSGITYKVELGVSE--ENELIVDPMENLYFTDRPPASVGVNGVTIHFMRIVVR 181
DB 121 LSMVRSMMGGIDKRVAAANTINGDFLVDPMENLYFTDRPPASVGVNGVTIHFMRIVVR 180
QY 182 ETLFARVFRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSBERTDLDITILLA 241
DB 181 ETLFASPIFANHPITIAARKFYFKPIDMGTEGGDFIVYDQQTVMVNGUSERTEAAINVL 240
QY 242 KNIKANKVEVEFKRIIVAINVPKWTNLMHLDTWLTMDKXKFLYSPANDVFKWDYDLVNG 301
DB 241 KXIQDSTSEFKRIIVINVPQLPNLMHLDTWLTMDKXKFLYSPNMLAVLAKWIDF-- 297
QY 302 GAEPQPOLNGL--PLDKLASIINKEPVLPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
DB 298 -TDPALKWNEIAGDLSTILHTIIQKPMPLIPAGADANQTEIDITHFDGTNYLTIPSV 356
QY 360 VIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRK 405
DB 357 VVGARNKLTHTOLEAAGVKVIAFKGNQLSLGMSARCMSPLVK 402

RESULT 7
Q6KI67 PRELIMINARY; PRT; 409 AA.
AC Q6KI67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN Name=arCA; OrderedLocusNames=MPOB2230;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,
RA Butler J., Calvo S., Elkins T., FitzGerald M.G., Hafez N.,
RA Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.,
RA Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RL Genome Res. 14:1447-1461(2004).
DR EMBL; AE017308; AAT27709.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
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DR InterPro; IPR003876; Arg_deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 409 AA; 47022 MW; 8A2FDF56914614D6 CRC64;

Query Match 46.5%; Score 986; DB 2; Length 409;
Best Local Similarity 48.4%; Pred. No. 2e-59;
Matches 198; Conservative 73; Mismatches 120; Indels 18; Gaps 7;

QY 11 IHVSEIGELETVLVHPEGREIDYITPARLDELLEFSAILESADARKEHQSFKVIMKDRGI 70
DB 8 INVSEIGELKVLHTFONELKYSPYRLDELLEFNVLEWREAKEHNEFIQKLSGV 67
QY 71 NVVELTDLVAETDYLASKAAKEEFTETLEETVPVLTEANKKAVRAFLLSKPTHEWVEFM 128
DB 68 EPVELTDLVAESFESSIKVNDFFIQVLDLTPILDGLTKQLLPFFLDIKHSTRKTIE 127
QY 129 FMMSGITKYELGVES-ENELIVDPNLYFRDPPASVNGVTHFMRYIVRRRETLFAR 187
DB 128 LMMSGITQDISIHIERELIIDPNLYFSRDNFISGNSVLIISNMKYKTRKRETIPTD 187
QY 188 FVRNHPKLVKTPYDPA---MKMPTEGGDVFIYNNETLVGVVSERTDLDITLLAKN 243
DB 188 FIFKHPLYKKVNMFAFERKDLNNQISIEGGDVLVYSKEILLIGISERTTMSAILEDLEN 247
QY 244 IKANKEVEFKRIVAINVPKWNLMLHDLTWLMDKNKFLYSPIANDVFKFW---DYDLV 299
DB 248 FKTKR-SFKKIYGEVFKMKNLMLHDLTWLMDYDKFIYSPNVLTDLKFEINLDYEKI 306
QY 300 NGGAEPQOLNGLPLDKLLASIIKEPVLIPIGGAGATEMEIARETNFDGNTYLAIKGL 359
DB 307 S-----SKELHA-SLSEFLKLIIGNDPILIPITGGKASQITTDIETNFVAANYLIRPGV 360
QY 360 VIGYDRNEKTKAALKAAGITVLPFHGNQLSLGMGNARCMSMPLSRKDVK 408
DB 361 VIGYRNRYETOKALEGHGVKKVIAFEGNQLSLGMGSSRCMSMPLIRSNLK 409

RESULT 8
Q6HP29 PRELIMINARY; PRT; 410 AA.
AC Q6HP29;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE Arginine deiminase (EC 3.5.3.6).
GN Name=arca; OrderedLocusNames=BT9727_0341;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of the Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDJB databases.
DR EMBL; AE017355; AAT58997.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
KW Complete proteome.
SQ SEQUENCE 410 AA; 46922 MW; E1FE4927484E42BD CRC64;

Query Match 33.4%; Score 708.5; DB 2; Length 410;
Best Local Similarity 40.2%; Pred. No. 2.2e-40;
Matches 166; Conservative 74; Mismatches 150; Indels 23; Gaps 9;

DR InterPro; IPR003876; Arg_deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 409 AA; 47022 MW; 8A2FDF56914614D6 CRC64;

Query Match 46.5%; Score 986; DB 2; Length 409;
Best Local Similarity 48.4%; Pred. No. 2e-59;
Matches 198; Conservative 73; Mismatches 120; Indels 18; Gaps 7;

QY 11 IHVSEIGELETVLVHPEGREIDYITPARLDELLEFSAILESADARKEHQSFKVIMKDRGI 70
DB 8 INVSEIGELKVLHTFONELKYSPYRLDELLEFNVLEWREAKEHNEFIQKLSGV 67
QY 71 NVVELTDLVAETDYLASKAAKEEFTETLEETVPVLTEANKKAVRAFLLSKPTHEWVEFM 128
DB 68 EPVELTDLVAESFESSIKVNDFFIQVLDLTPILDGLTKQLLPFFLDIKHSTRKTIE 127
QY 129 FMMSGITKYELGVES-ENELIVDPNLYFRDPPASVNGVTHFMRYIVRRRETLFAR 187
DB 128 LMMSGITQDISIHIERELIIDPNLYFSRDNFISGNSVLIISNMKYKTRKRETIPTD 187
QY 188 FVRNHPKLVKTPYDPA---MKMPTEGGDVFIYNNETLVGVVSERTDLDITLLAKN 243
DB 188 FIFKHPLYKKVNMFAFERKDLNNQISIEGGDVLVYSKEILLIGISERTTMSAILEDLEN 247
QY 244 IKANKEVEFKRIVAINVPKWNLMLHDLTWLMDKNKFLYSPIANDVFKFW---DYDLV 299
DB 248 FKTKR-SFKKIYGEVFKMKNLMLHDLTWLMDYDKFIYSPNVLTDLKFEINLDYEKI 306
QY 300 NGGAEPQOLNGLPLDKLLASIIKEPVLIPIGGAGATEMEIARETNFDGNTYLAIKGL 359
DB 307 S-----SKELHA-SLSEFLKLIIGNDPILIPITGGKASQITTDIETNFVAANYLIRPGV 360
QY 360 VIGYDRNEKTKAALKAAGITVLPFHGNQLSLGMGNARCMSMPLSRKDVK 408
DB 361 VIGYRNRYETOKALEGHGVKKVIAFEGNQLSLGMGSSRCMSMPLIRSNLK 409

RESULT 9
Q81111 PRELIMINARY; PRT; 410 AA.
AC Q81111;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN OrderedLocusNames=BC0406;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haseikorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE016999; AAP07446.1; -.
DR HSP; PI3981; IRXX.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 410 AA; 46980 MW; 3D3AE8489168BD73 CRC64;

Query Match 33.4%; Score 707.5; DB 2; Length 410;
Best Local Similarity 40.9%; Pred. No. 2.5e-40;
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVSEIGELETVLVHPEGREIDYITPARLDELLEFSAILESADARKEHQSFKVIMKDRGI 70
DB 5 IHVSEIGELQTVLLKRPGEVENLTPDYLOQLLFPDIPYLPYIQQEHDYFAQTLNRGV 64

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QY	71	NVVELTDLVAETDYLASKAAKEEFIEFTLEETVPLTEANKKAVRAFLSKPHEWVEFM	130
Db	65	EVLYLEKLAEEA--LVDKLREEFVDRILKEGQADVAVAH--QTLKEYLLSFSNEELIQKI	121
QY	131	MSGITK-----YELGVSENELIVDPMPNLYFTRDPAASVGDGLTINKMREPAR	179
Db	122	MGGVRKNEIETSKKTHLYEL--MEDHYPPYLDPMNLYFTRDPAASVGDGLTINKMREPAR	180
QY	180	RRETLFARFVRNHPKLVK--TPWYDYPAMKQPIEGGDVFIYNNETLVVGVSERTDLDTI	237
Db	181	RRESLFMEYIIKYHPRFAKNVPWLDRDYKFPFIEGGDELILNEETIAGVSARTSAKAI	240
QY	238	TLIAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP--IANDVFKWDY	296
Db	241	ERLAKNL--FSRQNKIKKVLAIKPCRAFPHLDTVFTMVDYDKFTIHPAIQPGKGNMNIY	299
QY	297	DLVNGGAEPQPOL--NGLPLDKLLASII--KEPVLIPIGGAGATEMEIARETNFPGTNYLA	354
Db	300	ILEKGSDEETLKITHRTSLMEALKEVLGSELVLIPOGGDV--IASAREQWNGDSNTLA	357
QY	355	IKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSMPLSRKDV	407
Db	358	IAPGVVVTYDRNVVNTLLREHGIEVIEVLSSELSRGRGPRCMSGMPIVRKDI	410
RESULT 10			
ID	Q73B87	PRELIMINARY; PRT; 410 AA.	
AC	Q73B87		
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	Arginine deiminase (EC 3.5.3.6).		
GN	Name=arcA;		
OS	Bacillus cereus (strain ATCC 10987);		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=222523;		
RN	SEQUENCE FROM N.A.		
RP	PubMed=14960714; DOI=10.1093/nar/gkh258;		
RA	Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,		
RA	Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,		
RA	Nelson W.C., Kistoe A.-B., Fraser C.M., Read T.D.;		
RT	"the genome sequence of Bacillus cereus ATCC 10987 reveals metabolic		
RT	adaptations and a large plasmid related to Bacillus anthracis pXO1."		
RL	Nucleic Acids Res. 32:1977-988 (2004).		
DR	EMBL; AE017265; AAS39407.1; -.		
DR	TIGR; BCE0472; -.		
DR	GO; GO:0016990; F:arginine deiminase activity; IEA.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0006527; P:arginine catabolism; IEA.		
DR	InterPro; IPR003199; Amidino.trans.		
DR	Pfam; PF02274; Amidinotransf. 1.		
DR	PRINTS; PR01466; ARGDEIMINASE.		
DR	TIGRFAMs; TIGR01078; arcA; 1.		
KW	Complete proteome; Hydrolase.		
SQ	SEQUENCE 410 AA; 46938 MW; 8D7846C8DD206579A CRC64;		
Query Match 33.3%; Score 705.5; DB 2; Length 410;			
Best Local Similarity 40.9%; Pred. No. 3.5e-40;			
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;			
QY	11	IHVSEIGELTVLHVEPGREIDYITPARLDELFSAILSHEDARKEHOSFVKIMDRGI	70
Db	5	IHVSEIGELQVLKRPKGEVENLTDPYLOQLLFDIDIPYLIQKHEHYFAQTLANRGV	64
QY	71	NVVELTDLVAETDYLASKAAKEEFIEFTLEETVPLTEANKKAVRAFLSKPHEWVEFM	130
Db	65	EVLYLEKLAEEA--LVDKLREEFVDRILKEGQADVAVAH--QTLKEYLLSFSNEELIQKI	121
QY	131	MSGITK-----YELGVSENELIVDPMPNLYFTRDPAASVGDGLTINKMREPAR	179

```
Db 240 EKLKII---AETDFKQVLAFAVIGENRKFHMLDTVFTTHIDYDKFTIHPDIEQGLKV--FS 294
QY 298 LVNGGAEPQQLNGLPLDKLLASINKEPV-LIPICGAGATEMEIARETNFDGTNYLAIK 356
Db 295 ITKGEMVPFVIELUTKLENVLAKALGLSVTLIPCG--GGDPVEAREQWNGDSNTLITA 352
QY 357 PCLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDV 407
Db 353 PGEVVVYDRNVVTNILEYKIGIKLRGSELVGRGGPRCNSMPFERNL 403

RESULT 12
Q8GG81 PRELIMINARY; PRT; 409 AA.
AC Q8GG81;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE AdS.
GN Name=adS;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I9841/1;
RA Winterhoff N., Goethe R., Gruening P., Valentin-Weigand P.;
RT "Identification and Characterization of Two Temperature-induced
RT Surface-associated Proteins of Streptococcus suis with High Homologies
RT to Members of the Arginine Deiminase System of Streptococcus
RT pyogenes.";
RL J. Bacteriol. 0:0-0(2002).
DR EMBL; AF546864; AAN76306.1; -.
DR HSSP; P13981; 1RXK.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; F:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR pfam; PF02274; Arg deiminase.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arcA; 1.
DR SEQUENCE 409 AA; 46345 MW; 4DCC04E37B40394C CRC64;

Query Match 32.2%; Score 682.5; DB 2; Length 409;
Best Local Similarity 39.4%; Pred. No. 1.3e-38;
Matches 164; Conservative 76; Mismatches 145; Indels 31; Gaps 12;

QY 11 IHVYSEIGELTVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS FVKIMKDRGI 70
Db 6 IHVFEIGKLVKMLHRRPGKSIENLMPDYLERLLPDDIPFLEDAQKEHDAFAQALRDGV 65
QY 71 NVVELTDLVAETDYDLASKAAKEEFETETLEETVPVLTEANKKAVRAFLLS-KPTHEMVFEF 129
Db 66 EVLYLEKLAASS--LVTPREIQFIDEXLEE-ANIRGRATKAIKRLMSIEDNQELVEK 122
QY 130 MMSGTKYKVELG-----VSENELIVDMPNLYFTDRPPASVGVNGVTIHFMYI 177
Db 123 TMAGVQKAE LPKI PSEKGLTDLVSESYFFALDMPNLYFTDRPPATIGNAVSLNHMYSE 182
QY 178 VRRRETLFARVFRNHPKL-VKTPWYDPAKMPLEGSDVFIYNNETLVGVGSERDLDIT 236
Db 183 TNRETLYGKIYFTHPEYGGKVPVLYNREETRIEGGDELVLSKDLAVAGISQRTDAAS 242
QY 237 ITLLAKNIKANKEVEFKRIVAINVVKWNTNLMHLDTWLMLDKNKFLYSP-IANDVFKP-- 293
Db 243 IEKLVNII-FERHVGFKVLAFEFANNRKFHMLDTVFTWVDYDKFTIHPTEGDLRVFSV 301
QY 294 -WDYDLVNGGAEPQQLNGLPLDKLLASINKEPV-LIPICGAGATEMEIARETNFDGTN 351
Db 302 TYENDTLHIEE-----HG-DLAELLAANUGLEKVELIRCCGGDM--VAAGREQWNGDSN 353
QY 352 YLAIKPGLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDV 407
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Db 354 TLTTPAGVVVVYKGRNTITNAILESKGLRIKIGSELVGRGGPRCNSMPFERDI 409

RESULT 13
Q62NR4 PRELIMINARY; PRT; 411 AA.
AC Q62NR4;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Arginine deiminase.
GN ORFNames=BU01912;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; CP000002; AAU25597.1; -.
DR SEQUENCE 411 AA; 47182 MW; 98BFE487FEC2C6E CRC64;

Query Match 32.1%; Score 681.5; DB 2; Length 411;
Best Local Similarity 38.4%; Pred. No. 1.5e-38;
Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;

QY 11 IHVYSEIGELTVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS FVKIMKDRGI 70
Db 5 IHVYSEIGLTKVLMKRPGRLENLTPYLERLLPDDIPFLPAVQKEHQDAETUKQQA 64
QY 71 NVVELTDLVAETDYDLASKAAKEEFETETLEETVPVLTEANKKAVRAFLLSKPTHEMVFEF 130
Db 65 EVLYLEKLTAEALDDA--LVREQFIDELLTESKADINGAYDR-LKEFLLTFDADSMVEQV 121
QY 131 MSGTKYKVELGVSENEL-----IVDMPNLYFTDRPPASVGVNGVTIHFMYIYVR 180
Db 122 MSGIRKNELEREKSHLHELMEDHYPFYLDMPNLYFTDRPPAAATGSLTINKKEPAR 181
QY 181 RETLFARVFRNHPKL--KTPWYDPAKMPLEGSDVFIYNNETLVGVGSERDLDIT 238
Db 182 RESLFMYIINHPRFKGHEIPVMLDRDFKFNIEGGDELVLNEETVAIGVSERTTAAIE 241
QY 239 LLAKNIKANKEVEFKRIVAINVVKWNTNLMHLDTWLMLDKNKFLYSPIANDVFKEDYDL 298
Db 242 RLVRNL-PQRSRIIRVLAIVEIPKSRAPMHLDTVFTWVDRDQFTIHPAQ----- 290
QY 299 VNGGAEPQQLNGLPLDKLLASINKEPVLP-----IGGAGATEMEIARE 344
Db 291 ---GPEGDMRIFVLERGKTADEIHTTEHNLPEVLKRTGLSLDVNLIFCGGDEIASARE 347
QY 345 TNFDGTNYLAIKPGVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSR 404
Db 348 QWNGDSNTLAPGVVVYDRNYISNECLREQIKVIEIPSGELSRGRGGRGRCNSMPLYR 407
QY 405 KDKV 408
Db 408 EDVK 411

RESULT 14
ARCA_BACLI
ID ARCA_BACLI STANDARD; PRT; 413 AA.
AC O86131;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).  
 GN Name=arcA;  
 OS Bacillus licheniformis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1402;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14580;  
 RX MEDLINE=99069319; PubMed=9851988;  
 RA Magnouj A, de Sousa Cabral T.F., Stalon V., Vander Wauwen C.;  
 RT "The arcABC gene cluster, encoding the arginine deiminase pathway of  
 RT Bacillus licheniformis, and its activation by the arginine repressor  
 RT argR";  
 RL J. Bacteriol. 180:6468-6475(1998).  
 CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
 CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- SIMILARITY: Belongs to the arginine deiminase family.  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; Y17554; CAA76777.1; -;  
 DR HAMAP; MF 00242; -; 1.  
 DR InterPro; IPR003198; Amidino trans.  
 DR InterPro; IPR003876; Arg.deiminase.  
 DR Pfam; PF02274; Amidinotransf; 1.  
 DR PRINTS; PR01466; ARGDEIMINASE.  
 DR TIGRFAMs; TIGR01078; arcA; 1.  
 DR Arginine metabolism; Hydrolase.  
 KW ACT\_SITE 402 402 Amidino-cysteine intermediate (By  
 FT similarity)  
 FT  
 SQ SEQUENCE 413 AA; 47427 MW; 57BB97714CAA5480 CRC64;  
 Query Match 32.1%; Score 681.5; DB 1; Length 413;  
 Best Local Similarity 38.4%; Pred. No. 1.5e-38;  
 Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;  
 QY 11 IHVSEIGETLVVHGEREIDYITPARLDELFSALLESHEHSHDARKEHQSFVKIMKDRGI 70  
 DB 7 IHVSEIGPLKTVMLKRPGELENLTPYLERLLFDDIPFLPAVQKEDQFAETLKQOGA 66  
 QY 71 NVVELTDLVAETYLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMVEFM 130  
 DB 67 EVLYLEKLTAEALDDA--LVREQFIDELTETSKADINGAYDR-LKEFLLTFDADSMVEQV 123  
 QY 131 MSGITKYELGVSENEL-----IVDPMPNLYFTRDPPFASVGVNGVTIHFMRIVYVR 180  
 DB 124 MSGIRKNELEREKSHLHELMEHDYFPYLDPMNLYFTRDPAAGISGLTIINCKKEPARR 183  
 QY 181 RETLFARFVFNHPKLV--KTPWYDYDPAMKMPTEGGDVFIYNNETLVGVGSRTDLDIT 238  
 DB 184 RESLFMYIINHHPFKGHEIPVWLRDQFKNIEGGDELVLNEETVAIGVSERTTAQAE 243  
 QY 239 LLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMQKPKLYSPIANDVFKFWDYDL 298  
 DB 244 RLVRNL-FQQRIRRVLAIVEIPKSRAPMHLDTVFTWDRDQFTIHPAQI----- 292  
 QY 299 VNGGAEPQOLNGLPLDKLLASIIINKEPVLIP-----IGGAGATEMEIARE 344  
 DB 293 ---GPEGDMRIFVLERGKTADEIHTTEHNLPEVLKRTGLSDVNLIFCGGDEIASARE 349  
 QY 345 TNFDGTNYLAKPGLVIGYDRNEKTNAALKAAGITVLPFHGNQLSLGMGNARCMSPILSR 404  
 DB 350 QWNGDSNTLALAPGVVVYTDYRNYISNECLREQGKIVIEIPSGELSRGGRGRCMSPILSR 409  
 QY 405 KDKV 408  
 DB 410 EDVK 413

Db 410 EDVK 413  
 RESULT 15  
 Q65D88 PRELIMINARY; PRT; 413 AA.  
 ID Q65D88  
 AC Q65D88; 28, Created  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 GN Arginine deiminase (EC 3.5.3.6).  
 GN ORFNames=Bli04163;  
 OS Bacillus licheniformis DSM 13.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=279010;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 13;  
 RX PubMed=15383718;  
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,  
 RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,  
 RA Ehrenreich A., Gottschalk G.;  
 RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an  
 RT Organism with Great Industrial Potential.";  
 RT J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
 DR EMBL; AE017333; AAU42976.1; -;  
 KW Hydrolase.  
 SQ SEQUENCE 413 AA; 47427 MW; 57BB97714CAA5480 CRC64;  
 Query Match 32.1%; Score 681.5; DB 2; Length 413;  
 Best Local Similarity 38.4%; Pred. No. 1.5e-38;  
 Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;  
 QY 11 IHVSEIGETLVVHGEREIDYITPARLDELFSALLESHEHSHDARKEHQSFVKIMKDRGI 70  
 DB 7 IHVSEIGPLKTVMLKRPGELENLTPYLERLLFDDIPFLPAVQKEDQFAETLKQOGA 66  
 QY 71 NVVELTDLVAETYLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMVEFM 130  
 DB 67 EVLYLEKLTAEALDDA--LVREQFIDELTETSKADINGAYDR-LKEFLLTFDADSMVEQV 123  
 QY 131 MSGITKYELGVSENEL-----IVDPMPNLYFTRDPPFASVGVNGVTIHFMRIVYVR 180  
 DB 124 MSGIRKNELEREKSHLHELMEHDYFPYLDPMNLYFTRDPAAGISGLTIINCKKEPARR 183  
 QY 181 RETLFARFVFNHPKLV--KTPWYDYDPAMKMPTEGGDVFIYNNETLVGVGSRTDLDIT 238  
 DB 184 RESLFMYIINHHPFKGHEIPVWLRDQFKNIEGGDELVLNEETVAIGVSERTTAQAE 243  
 QY 239 LLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMQKPKLYSPIANDVFKFWDYDL 298  
 DB 244 RLVRNL-FQQRIRRVLAIVEIPKSRAPMHLDTVFTWDRDQFTIHPAQI----- 292  
 QY 299 VNGGAEPQOLNGLPLDKLLASIIINKEPVLIP-----IGGAGATEMEIARE 344  
 DB 293 ---GPEGDMRIFVLERGKTADEIHTTEHNLPEVLKRTGLSDVNLIFCGGDEIASARE 349  
 QY 345 TNFDGTNYLAKPGLVIGYDRNEKTNAALKAAGITVLPFHGNQLSLGMGNARCMSPILSR 404  
 DB 350 QWNGDSNTLALAPGVVVYTDYRNYISNECLREQGKIVIEIPSGELSRGGRGRCMSPILSR 409  
 QY 405 KDKV 408  
 DB 410 EDVK 413  
 Search completed: April 6, 2005, 06:26:25  
 Job time : 185 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:04 ; Search time 174 Seconds  
(without alignments)  
909.109 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120  
Sequence: 1 MSVFDKFNHGVSEIGEL.....LGMGNARCMSPLSRKDKVKW 409

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	100.0	409	5	Aae16134 Mycoplasma
2	2120	100.0	409	5	Abg311996 M. hominu
3	2120	100.0	409	8	Adp79607 Mycoplasma
4	2116	99.8	409	8	Adp79608 Mycoplasma
5	2112	99.6	409	5	Aae16136 Mycoplasma
6	2112	99.6	409	8	Adp79609 Mycoplasma
7	2110	99.5	409	5	Aae16135 Mycoplasma
8	2109	99.5	408	2	Aaw89442 Mycoplasma
9	2108	99.4	409	5	Aae16137 Mycoplasma
10	2108	99.4	409	8	Adp79610 Mycoplasma
11	1807.5	85.3	410	5	Abg311995 M. arthri
12	1797.5	84.8	409	8	Adp79613 Mycoplasma
13	1796.5	84.7	409	2	Aaw89441 Mycoplasma
14	1793.5	84.6	409	8	Adp79616 Mycoplasma
15	1793.5	84.6	409	8	Adp79615 Mycoplasma
16	1789.5	84.4	409	8	Adp79614 Mycoplasma
17	1764.5	83.2	410	5	Abg311994 M. argini
18	1764.5	83.2	410	8	Adp79611 Mycoplasma
19	1763.5	83.2	410	5	Abb76127 Mycoplasma
20	1760.5	83.0	410	8	Adp79612 Mycoplasma
21	1753.5	82.7	409	2	Aaw89440 Mycoplasma
22	1733.5	81.8	409	2	Aar24528 Arginine
23	1732.5	81.7	410	2	Aaw65454 Arginine
24	1632.5	77.0	405	2	Aar05713 Arginine
25	1081.5	51.0	264	2	AAR20500 Cell grow

26	1067.5	50.4	263	2	AAR10854 Arginine
27	707.5	33.4	410	8	AdS27663 Bacterial
28	682.5	32.2	432	8	Adm77935 S. suis A
29	681.5	32.1	413	5	Abg32003 B. lichen
30	681.5	32.1	413	8	Adp79625 Bacillus
31	679	32.0	411	1	Adp70278 Streptoco
32	679	32.0	411	5	Abp26975 Streptoco
33	679	32.0	411	5	Abg31997 S. pyogen
34	679	32.0	411	7	AdC56694 Streptoco
35	679	32.0	411	8	Adp79619 Streptoco
36	678.5	32.0	410	5	Abp26974 Streptoco
37	670.5	31.6	408	5	Abg32004 E. faecal
38	670.5	31.6	408	8	Adp79626 Enterococ
39	667.5	31.5	417	7	AdC96521 E. faeciu
40	655	30.9	413	5	Abg32002 C. perfr
41	655	30.9	413	8	Adp79624 Clostridi
42	652.5	30.8	409	8	Adk47759 Streptoco
43	652.5	30.8	413	8	AdR94569 Novel S.
44	651.5	30.7	409	5	Abg31998 S. pneumo
45	651.5	30.7	409	6	ABU02672 S. pneumo

ALIGNMENTS

RESULT 1  
AAE16134  
ID AAE16134 standard; protein; 409 AA.  
XX  
AC AAE16134;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mycoplasma hominis wild type arginine deiminase (ADI).  
XX  
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour.  
XX  
OS Mycoplasma hominis.  
XX  
PN WO200183774-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014116.  
XX  
PR 04-MAY-2000; 2000US-00564559.  
XX  
PI (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Ensor CM, Holtsberg FW, Clark MA;  
XX  
DR WPI; 2002-097497/13.  
XX  
PT Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
PS Example 3; Fig 1; 34pp; English.  
XX  
CC The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis wild type ADI  
SQ Sequence 409 AA;

Query Match 100.0%; Score 2120; DB 5; Length 409;

Best Local Similarity 100.0%; Pred. No. 1.5e-193;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKNGIHVYSEIGELTDLVHPGRIIDYITPARLDELFSALLESKDARKHQH 60  
DB 1 MSVFDKNGIHVYSEIGELTDLVHPGRIIDYITPARLDELFSALLESKDARKHQH 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLEETVPVLTANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLEETVPVLTANKKAVRAFLLS 120

QY 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYTRDPFASVGNVGTTHFMYIIVRR 180  
DB 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYTRDPFASVGNVGTTHFMYIIVRR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240  
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240

QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300

QY 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
DB 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVL 360

QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409  
DB 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409

RESULT 2  
ABG31996  
ID ABG31996 standard; protein; 409 AA.  
XX AC ABG31996;  
XX DT 06-AUG-2003 (revised)  
XX DT 15-NOV-2002 (first entry)  
XX DE M. hominus arginine deiminase gene, HOMADIPRO.  
XX KW Arginine deiminase; cytostatic; ADI; polyethylene glycol; PEG; arginine;  
XX KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;  
XX KW auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.  
XX OS Mycoplasma hominis.  
XX PN WO200244360-A2.  
XX PD 06-JUN-2002.  
XX PF 19-SEP-2001; 2001WO-US029184.  
XX PR 28-NOV-2000; 2000US-00723546.  
XX PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX PI Clark MA;  
XX WP1; 2002-619003/66.  
XX PT Compound for treating tumor such as melanoma, hepatoma or sarcoma in a  
XX PT patient, comprises arginine deiminase covalently bonded by a linking  
XX PT group such as succinimide to polyethylene glycol.  
XX PS Example 1; Fig 1; 59pp; English.  
XX CC The invention discloses a compound comprising arginine deiminase (ADI)  
XX CC covalently bonded by a linking group to polyethylene glycol (PEG) having  
XX CC a total weight average molecular weight of about 1000-50000. Also  
XX CC disclosed is a method for enhancing the circulating half life or the

tumouricidal activity of arginine deiminase by modifying the arginine  
deiminase by covalently bonding the arginine deiminase by a linking group  
to PEG. Normal cells can synthesise arginine from citrulline in a 2 step  
process catalysed by argininosuccinate synthase and argininosuccinate  
lyase. In contrast, many cancerous cells do not express argininosuccinate  
synthase and are, therefore, auxotrophic for arginine. Arginine deiminase  
catalyses the conversion of arginine to citrulline and can be used to  
eliminate arginine from the cancerous cells. The compound is useful for  
treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or  
for treating and inhibiting metastases in a patient. When compared to  
native arginine deiminase the compound retains most of its enzymatic  
activity, is far less antigenic, has a greatly extended circulating half-  
life, and is much more efficacious in the treatment of tumours. The  
sequence presented is the Mycoplasma hominus arginine deiminase gene,  
CC HOMADIPRO. (Updated on 06-AUG-2003 to correct OS field.)  
XX

Sequence 409 AA;

Query Match 100.0%; Score 2120; DB 5; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.5e-193;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKNGIHVYSEIGELTDLVHPGRIIDYITPARLDELFSALLESKDARKHQH 60  
DB 1 MSVFDKNGIHVYSEIGELTDLVHPGRIIDYITPARLDELFSALLESKDARKHQH 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLEETVPVLTANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLEETVPVLTANKKAVRAFLLS 120

QY 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYTRDPFASVGNVGTTHFMYIIVRR 180  
DB 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYTRDPFASVGNVGTTHFMYIIVRR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240  
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240

QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300

QY 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
DB 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVL 360

QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409  
DB 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409

RESULT 3  
ADP79607  
ID ADP79607 standard; protein; 409 AA.  
XX AC ADP79607;  
XX DT 04-NOV-2004 (first entry)  
XX DE Mycoplasma hominis arginine deiminase.  
XX KW Arginine deiminase; cytostatic; virucide; viral replication;  
XX KW nitric oxide synthesis; tumour; liver function; enzyme.  
XX OS Mycoplasma hominis.  
XX PN WO2004046309-A2.  
XX PD 03-JUN-2004.  
XX PF 29-SEP-2003; 2003WO-US030770.  
XX PR 18-NOV-2002; 2002US-0427497P.

XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX Clark MA;  
XX WPI; 2004-431965/40.  
XX Inhibiting replication of viruses in individual, involves administering  
XX composition comprising arginine deiminase bonded to polyethylene glycol,  
XX to individual.  
XX  
XX Claim 18; SEQ ID NO 1; 89pp; English.  
XX  
XX The invention relates to inhibiting the replication of one or more  
XX viruses in an individual and involves administering to the individual a  
XX composition comprising an arginine deaminase bonded to polyethylene  
XX glycol. The method is useful for inhibiting replication of one or more  
XX viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
XX where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
XX M. hominis, M. arthritidis and its combination. It is useful for treating  
XX an individual who is suspected of having been exposed to one or more  
XX viruses, for modulating nitric oxide levels in an individual, or for  
XX selectively inhibiting viral replication in an individual. The method is  
XX also useful for treating a tumour and inhibiting replication of one ore  
XX more viruses in an individual. The tumour is melanoma, sarcoma, or  
XX hepatoma. The tumour is hepatocellular carcinoma. The method is also  
XX useful for improving liver function in an individual. The present  
XX sequence represents a Mycoplasma hominis arginine deaminase.  
XX  
SQ Sequence 409 AA;  
  
Query Match 100.0%; Score 2120; DB 8; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.5e-193;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MSVFDKFNHIVYSEIGELTDLVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 60  
Db 1 MSVFDKFNHIVYSEIGELTDLVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 60  
  
Qy 61 FVKIMKORGINNVETLDVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 120  
Db 61 FVKIMKORGINNVETLDVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 120  
  
Qy 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNPYLFTRDPPFASVGNVGTIHFMYIYVR 180  
Db 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNPYLFTRDPPFASVGNVGTIHFMYIYVR 180  
  
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITILL 240  
  
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDITWLTMLDKNKFYSPDIANDVKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDITWLTMLDKNKFYSPDIANDVKFWDYDLVN 300  
  
Qy 301 GGAEPQQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFGTNYLAIKPGIV 360  
Db 301 GGAEPQQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFGTNYLAIKPGIV 360  
  
Qy 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409  
Db 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409  
  
RESULT 4  
ADP79608  
ID ADP79608 standard; protein; 409 AA.  
XX  
AC ADP79608;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Mycoplasma hominis arginine deaminase variant.

XX Arginine deaminase; cytostatic; virucide; viral replication;  
XX nitric oxide synthesis; tumour; liver function; enzymes; variant.  
XX Mycoplasma hominis.  
XX  
XX Key Location/Qualifiers  
XX Misc-difference 112 /label= K112E  
XX /note= "wild-type Lys is substituted with with Glu"  
XX  
XX W02004046309-A2.  
XX  
XX 03-JUN-2004.  
XX  
XX 29-SEP-2003; 2003WO-US030770.  
XX  
XX 18-NOV-2002; 2002US-0427497P.  
XX  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX Clark MA;  
XX WPI; 2004-431965/40.  
XX  
XX Inhibiting replication of viruses in individual, involves administering  
XX composition comprising arginine deiminase bonded to polyethylene glycol,  
XX to individual.  
XX  
XX Claim 18; SEQ ID NO 2; 89pp; English.  
XX  
XX The invention relates to inhibiting the replication of one or more  
XX viruses in an individual and involves administering to the individual a  
XX composition comprising an arginine deaminase bonded to polyethylene  
XX glycol. The method is useful for inhibiting replication of one or more  
XX viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
XX where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
XX M. hominis, M. arthritidis and its combination. It is useful for treating  
XX an individual who is suspected of having been exposed to one or more  
XX viruses, for modulating nitric oxide levels in an individual, or for  
XX selectively inhibiting viral replication in an individual. The method is  
XX also useful for treating a tumour and inhibiting replication of one ore  
XX more viruses in an individual. The tumour is melanoma, sarcoma, or  
XX hepatoma. The tumour is hepatocellular carcinoma. The method is also  
XX useful for improving liver function in an individual. The present  
XX sequence represents a Mycoplasma hominis arginine deaminase variant.  
XX  
SQ Sequence 409 AA;  
  
Query Match 99.8%; Score 2116; DB 8; Length 409;  
Best Local Similarity 99.8%; Pred. No. 3.5e-193;  
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MSVFDKFNHIVYSEIGELTDLVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 60  
Db 1 MSVFDKFNHIVYSEIGELTDLVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 60  
  
Qy 61 FVKIMKORGINNVETLDVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 120  
Db 61 FVKIMKORGINNVETLDVAETYLDAKAAKEEFTETFLTEETVPVLTANKKAVRAFLLS 120  
  
Qy 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNPYLFTRDPPFASVGNVGTIHFMYIYVR 180  
Db 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNPYLFTRDPPFASVGNVGTIHFMYIYVR 180  
  
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITILL 240  
  
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDITWLTMLDKNKFYSPDIANDVKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDITWLTMLDKNKFYSPDIANDVKFWDYDLVN 300

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Qy 301 GGAEPPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
Db 301 GGAEPPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLSGMGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLSGMGNARCMSPLSRKDVKW 409

RESULT 5
AAE16136
ID AAE16136 standard; protein; 409 AA.
AC AAE16136;
XX
DT 26-MAR-2002 (first entry)
XX
DE Mycoplasma hominis modified arginine deiminase (ADI) #2.
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;
KW septic shock; tumour; mutant; mutein.
XX
OS Mycoplasma hominis.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Pro substituted with Ser"
FN WO200183774-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014116.
XX
PR 04-MAY-2000; 2000US-00564559.
XX
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX
PI Ensor CM, Holtsberg FW, Clark MA;
XX
DR WPI; 2002-097497/13.
XX
CC The invention relates to a modified arginine deiminase (ADI) for improved
CC manufacturing processes. The process comprises ADI modified to be free of
CC at least one pegylation site at or adjacent to its catalytic region. ADI
CC catalyses the conversion of arginine to citrulline and may be used to
CC eliminate arginine. ADI is useful for treating cancer, melanomas,
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating
CC and inhibiting metastasis of tumour cells and other disease states. The
CC present sequence is Mycoplasma hominis modified ADI protein
XX
SQ Sequence 409 AA;

Query Match 99.6%; Score 2112; DB 5; Length 409;
Best Local Similarity 99.8%; Pred No. 8, 5e-193;
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSVFDSEKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFLPSAILESHDARKHQ 60
Db 1 MSVFDSEKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFLPSAILESHDARKHQ 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYLSKAAKEEFTETLEETVPVLTEANKKAVRAFLLS 120
Db 61 FVKIMKDRGINVVELTDLVAETDYLSKAAKEEFTETLEETVPVLTEANKKAVRAFLLS 120
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Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMYIIVRR 180
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMYIIVRR 180
Qy 181 RETLPAFVFRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVGVSERTDLDITLL 240
Db 181 RETLPAFVFRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVGVSERTDLDITLL 240
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300
Qy 301 GGAEPPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
Db 301 GGAEPPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLSGMGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLSGMGNARCMSPLSRKDVKW 409

RESULT 6
ADP79609
ID ADP79609 standard; protein; 409 AA.
XX
AC ADP79609;
XX
DT 04-NOV-2004 (first entry)
XX
DE Mycoplasma hominis arginine deiminase variant.
KW Arginine deiminase; cytostatic; virucide; viral replication;
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.
XX
OS Mycoplasma hominis.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /label= P210S
FT /note= "wild-type Pro is substituted with Ser"
XX
FN WO2004046309-A2.
XX
PD 03-JUN-2004.
XX
PF 29-SEP-2003; 2003WO-US030770.
XX
PR 18-NOV-2002; 2002US-0427497P.
XX
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX
PI Clark MA;
XX
DR WPI; 2004-431965/40.
XX
PT Inhibiting replication of viruses in individual, involves administering
PT composition comprising arginine deiminase bonded to polyethylene glycol,
PT to individual.
XX
PS Claim 18; SEQ ID NO 3; 89pp; English.
XX

The invention relates to inhibiting the replication of one or more
viruses in an individual and involves administering to the individual a
composition comprising an arginine deiminase bonded to polyethylene
glycol. The method is useful for inhibiting replication of one or more
viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,
where the arginine deiminase is derived from Mycoplasma e.g. M. arginini,
M. hominis, M. arthritidis and its combination. It is useful for treating
an individual who is suspected of having been exposed to one or more
viruses, for modulating nitric oxide levels in an individual, or for
selectively inhibiting viral replication in an individual. The method is
also useful for treating a tumour and inhibiting replication of one ore
more viruses in an individual. The tumour is melanoma, sarcoma, or
```



CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma hominis arginine deaminase variant.  
XX  
SQ Sequence 409 AA;  
  
Query Match 99.6%; Score 2112; DB 8; Length 409;  
Best Local Similarity 99.8%; Pred. No. 8.5e-193;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MSVFSKFNHGVSEIGLETLVHVEPGREIDYITPARLDELLSFAILESHDARKEHQ 60  
DB 1 MSVFSKFNHGVSEIGLETLVHVEPGREIDYITPARLDELLSFAILESHDARKEHQ 60  
  
QY 61 FVKMKDRGINVVELTDLVAETDYLASKAAKEEFTEETVPVLTTEANKKAVRAFLLS 120  
DB 61 FVKMKDRGINVVELTDLVAETDYLASKAAKEEFTEETVPVLTTEANKKAVRAFLLS 120  
  
QY 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVGTIHFMYIYVR 180  
DB 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVGTIHFMYIYVR 180  
  
QY 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGSERTDLDITILL 240  
DB 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGSERTDLDITILL 240  
  
QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
  
QY 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
DB 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
  
QY 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 409  
DB 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 409  
  
RESULT 7  
AAE16135  
ID AAE16135 standard; protein; 409 AA.  
XX  
AC AAE16135;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mycoplasma hominis modified arginine deiminase (ADI) #1.  
XX  
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour; mutant; mutein.  
XX  
OS Mycoplasma hominis.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 111  
FT /note= "Wild type Lys substituted with Pro"  
FT Misc-difference 112  
FT /note= "Wild type Lys substituted with Glu"  
XX  
PN WO200183774-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014116.  
XX  
PR 04-MAY-2000; 2000US-00564559.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Ensor CM, Holtsberg FW, Clark MA;

XX WPI; 2002-097497/13.  
XX Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
PS Disclosure; Page 30-31; 34pp; English.  
XX  
CC The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis modified ADI protein  
XX  
SQ Sequence 409 AA;  
  
Query Match 99.5%; Score 2110; DB 5; Length 409;  
Best Local Similarity 99.5%; Pred. No. 1.3e-192;  
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MSVFSKFNHGVSEIGLETLVHVEPGREIDYITPARLDELLSFAILESHDARKEHQ 60  
DB 1 MSVFSKFNHGVSEIGLETLVHVEPGREIDYITPARLDELLSFAILESHDARKEHQ 60  
  
QY 61 FVKMKDRGINVVELTDLVAETDYLASKAAKEEFTEETVPVLTTEANKKAVRAFLLS 120  
DB 61 FVKMKDRGINVVELTDLVAETDYLASKAAKEEFTEETVPVLTTEANKKAVRAFLLS 120  
  
QY 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVGTIHFMYIYVR 180  
DB 121 KPTHEWVFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVGTIHFMYIYVR 180  
  
QY 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGSERTDLDITILL 240  
DB 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGSERTDLDITILL 240  
  
QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
  
QY 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
DB 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
  
QY 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 409  
DB 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 409  
  
RESULT 8  
AAW89442  
ID AAW89442 standard; protein; 408 AA.  
XX  
AC AAW89442;  
XX  
DT 18-MAR-1999 (first entry)  
XX  
DE Mycoplasma hominis arginine deiminase.  
XX  
KW Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritis;  
KW Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;  
KW inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.  
XX  
OS Mycoplasma hominis.  
XX  
PN WO9851784-A1.  
XX  
PD 19-NOV-1998.  
XX

PF 12-MAY-1998; 98WO-US009575.  
 XX  
 PR 12-MAY-1997; 97US-0046200P.  
 PR 13-FEB-1998; 98US-00023809.  
 XX  
 PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
 XX  
 PI Clark MA;  
 XX  
 DR WPI; 1999-045227/04.  
 XX  
 PT New compound comprising arginine deiminase - covalently bonded via  
 PT linking group to polyethylene glycol, to enhance the half life of  
 PT arginine by this modification.  
 XX  
 PS Claim 6; Fig 1; 30pp; English.  
 XX  
 CC The present sequence represents Mycoplasma hominis arginine deiminase.  
 CC The present invention describes: (1) a compound comprising arginine  
 CC deiminase (AD) covalently bonded via linking group to polyethylene glycol  
 CC (PEG), and having a molecular weight 12-40 kDa; and (2) a composition as  
 CC above, but where the linking group is selected from a malimide group, an  
 CC amide group, an imide group, a carbamate group, an ester group, an epoxy  
 CC group, a carboxyl group, a hydroxyl group, a carboxylate, a tyrosine  
 CC group, a cysteine group and/or a histidine group. AD can be used in the  
 CC treatment of tumours, e.g. melanomas, hepatomas and sarcomas, and to  
 CC inhibit metastasis. The modified AD has an enhanced circulating half life  
 XX  
 SQ Sequence 408 AA;

Query Match 99.5%; Score 2109; DB 2; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-192;  
 Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFSKFNHIVYSEIGLETVLHVEPGREIDYITPARDELLESAILESHEQHS 60  
 DB 1 MSVFSKFNHIVYSEIGLETVLHVEPGREIDYITPARDELLESAILESHEQHS 60

QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120  
 DB 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120

QY 121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180  
 DB 121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVVGVSERTDITILL 240  
 DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVVGVSERTDITILL 240

QY 241 AKNIKANKEVEFKRIIVAINVPRKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLVN 300  
 DB 241 AKNIKANKEVEFKRIIVAINVPRKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLVN 300

QY 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360  
 DB 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360

QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
 DB 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408

RESULT 9  
 AAEL6137  
 ID AAEL6137 standard; protein; 409 AA.  
 XX  
 AC AAEL6137;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Mycoplasma hominis modified arginine deiminase (ADI) E112, S210.  
 XX

KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
 KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
 KW septic shock; tumour; mutant; mutein.  
 OS Mycoplasma hominis.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 112 /note= "Wild type Lys substituted with Glu"  
 FT Misc-difference 210 /note= "Wild type Pro substituted with Ser"  
 FT  
 XX  
 PN WO200183774-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014116.  
 XX  
 PR 04-MAY-2000; 2000US-00564559.  
 XX  
 PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
 XX  
 PI Ensor CM, Holtsberg FW, Clark MA;  
 XX  
 DR WPI; 2002-097497/13.  
 XX  
 PT Modified arginine deiminase for improved manufacturing processes and for  
 PT treating cancer, is mutated to be free of a pegylation site at or  
 PT adjacent to its catalytic region.  
 XX  
 PS Example 1; Fig 2; 34pp; English.  
 XX  
 CC The invention relates to a modified arginine deiminase (ADI) for improved  
 CC manufacturing processes. The process comprises ADI modified to be free of  
 CC at least one pegylation site at or adjacent to its catalytic region. ADI  
 CC catalyses the conversion of arginine to citrulline and may be used to  
 CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
 CC hepatomas, sarcomas, parasitic diseases, septic shock, and for treating  
 CC and inhibiting metastasis of tumour cells and other disease states. The  
 CC present sequence is Mycoplasma hominis modified ADI protein  
 XX  
 SQ Sequence 409 AA;

Query Match 99.4%; Score 2108; DB 5; Length 409;  
 Best Local Similarity 99.5%; Pred. No. 2e-192;  
 Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVFSKFNHIVYSEIGLETVLHVEPGREIDYITPARDELLESAILESHEQHS 60  
 DB 1 MSVFSKFNHIVYSEIGLETVLHVEPGREIDYITPARDELLESAILESHEQHS 60

QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120  
 DB 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120

QY 121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180  
 DB 121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVVGVSERTDITILL 240  
 DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVVGVSERTDITILL 240

QY 241 AKNIKANKEVEFKRIIVAINVPRKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLVN 300  
 DB 241 AKNIKANKEVEFKRIIVAINVPRKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLVN 300

QY 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360  
 DB 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360

QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

Db 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLGNGNARCMSPLSRKDKVKW 409

RESULT 10  
ADP79610  
ID ADP79610 standard; protein; 409 AA.  
XX  
AC ADP79610;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Mycoplasma hominis arginine deaminase variant.  
XX  
KW Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
OS Mycoplasma hominis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 112 /label= K112E  
FT /note= "wild-type Lys is substituted with with Glu"  
FT Misc-difference 210 /label= P210S  
FT /note= "wild-type Pro is substituted with with Ser"  
XX  
PN WO2004046309-A2.  
XX  
PD 03-JUN-2004.  
XX  
PF 29-SEP-2003; 2003WO-US030770.  
XX  
PR 18-NOV-2002; 2002US-0427497P.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
DR WPI; 2004-431965/40.  
XX  
PT Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
PS Claim 18; SEQ ID NO 4; 89pp; English.  
XX  
CC The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritidis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma hominis arginine deaminase variant.  
XX  
SQ Sequence 409 AA;

Query Match 99.4%; Score 2108; DB 8; Length 409;  
Best Local Similarity 99.5%; Pred. No. 2e-192;  
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSVPSKNGIHVYSEIGELETVLVHEPGREIDYITPARDELLESAILSHDARKEHQS 60  
Db 1 MSVPSKNGIHVYSEIGELETVLVHEPGREIDYITPARDELLESAILSHDARKEHQS 60

Qy 61 FVKIMKORGINNVVELTDLVAETYDLASKAAKEEFTEFTLEETVPVLTBANKKAVRAFLLS 120  
Db 61 FVKIMKORGINNVVELTDLVAETYDLASKAAKEEFTEFTLEETVPVLTBANKKAVRAFLLS 120  
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDMPNLYFTRDPASVGVNGVTTHFMYIYVR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDMPNLYFTRDPASVGVNGVTTHFMYIYVR 180  
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGSDVFIYNNETLVVGVSERTDLDITILL 240  
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVN 300  
Qy 301 GGAEPQOLNGLPLDKLIASIIINKEPVLIPIGGAGATEMETARETNFDGTNYLAIKPGLV 360  
Db 301 GGAEPQOLNGLPLDKLIASIIINKEPVLIPIGGAGATEMETARETNFDGTNYLAIKPGLV 360  
Qy 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLGNGNARCMSPLSRKDKVKW 409  
Db 361 IGYDRNEKTNAAALKAAGITVLPFHGNQSLGNGNARCMSPLSRKDKVKW 409  
RESULT 11  
ABG31995  
ID ABG31995 standard; protein; 410 AA.  
XX AC ABG31995;  
XX DT 15-NOV-2002 (first entry)  
XX DE M. arthritidis arginine deiminase gene, ARTADIPRO.  
XX KW Arginine deiminase; cytostatic; ADI; polyethylene glycol; PEG; arginine;  
KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;  
KW auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.  
XX OS Mycoplasma arthritidis.  
XX PN WO200244360-A2.  
XX PD 06-JUN-2002.  
XX PF 19-SEP-2001; 2001WO-US029184.  
XX PR 28-NOV-2000; 2000US-00723546.  
XX PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX PI Clark MA;  
XX WPI; 2002-619003/66.  
XX Compound for treating tumor such as melanoma, hepatoma or sarcoma in a  
XX patient, comprises arginine deiminase covalently bonded by a linking  
XX group such as succinimide to polyethylene glycol.  
XX Example 1; Fig 1; 59pp; English.  
XX The invention discloses a compound comprising arginine deiminase (ADI)  
XX covalently bonded by a linking group to polyethylene glycol (PEG) having  
XX a total weight average molecular weight of about 1000-50000. Also  
XX disclosed is a method for enhancing the circulating half life or the  
XX tumoricidal activity of arginine deiminase by modifying the arginine  
XX deiminase by covalently bonding the arginine deiminase by a linking group  
XX to PEG. Normal cells can synthesize arginine from citrulline in a 2 step  
XX process catalysed by argininosuccinate synthase and argininosuccinate  
XX lyase. In contrast, many cancerous cells do not express argininosuccinate  
XX synthase and are, therefore, auxotrophic for arginine. Arginine deiminase  
XX catalyses the conversion of arginine to citrulline and can be used to  
XX eliminate arginine from the cancerous cells. The compound is useful for



XX 19-NOV-1998.  
XX 12-MAY-1998; 98WO-US009575.  
XX 12-MAY-1997; 97US-0046200P.  
PR 13-FEB-1998; 98US-00023809.  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
FA Clark MA;  
PI WPI; 1999-045227/04.  
XX  
XX New compound comprising arginine deiminase - covalently bonded via  
PT linking group to polyethylene glycol, to enhance the half life of  
PT arginine by this modification.  
XX  
XX Claim 6; Fig 1; 30pp; English.  
XX  
XX The present sequence represents Mycoplasma arthritis arginine  
CC deiminase. The present invention describes: (1) a compound comprising  
CC arginine deiminase (AD) covalently bonded via linking group to  
CC polyethylene glycol (PEG), and having a molecular weight 12-40 kDa; and  
CC (2) a composition as above, but where the linking group is selected from  
CC a malimide group, an amide group, an imide group, a carbamate group, an  
CC ester group, an epoxy group, a carboxyl group, a hydroxyl group, a  
CC carbohydrate, a tyrosine group, a cysteine group and/or a histidine  
CC group. AD can be used in the treatment of tumours, e.g. melanomas,  
CC hepatomas and sarcomas, and to inhibit metastasis. The modified AD has an  
CC enhanced circulating half life  
XX  
XX Sequence 409 AA;  
Query Match 84.7%; Score 1796.5; DB 2; Length 409;  
Best Local Similarity 84.4%; Pred. No. 1.3e-162; Mismatches 34; Indels 1; Gaps 1;  
Matches 345; Conservative 29;  
QY 1 MSVFDKFGNHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
DB 1 MSVFDKFGNHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
QY 61 FVKMKRGINVELTDLVAETDYDLASAKAEETFTLEETVPLTANKKAVRAFLLS 120  
DB 61 FVAILKANDINNVETIDLVAETDYDLASQAEKDRLEEFLEDEPVLSEAHKVVNFLLKA 120  
QY 121 KPT-HEMVDFWMSGITKYELGVSENELIVDPMNLYETRDPPFASVGVNGVTIHFMYIVR 179  
DB 121 KKTSRKLVLMWAGITKYDVGAEADHELIYDPMNLYETRDPPFASVGVNGVTIHFMYIVR 180  
QY 180 RRETLFARFVFNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239  
DB 181 RRETLFARFVFNHPKLVNTWYDPAKMLSTEGGDVFIYNNETLVVGVSERTDLDITL 240  
QY 240 LAKNIKANKEVEFKRIVAINVVKWNTLMHLDLWTLMDKNKFLYSPIANVDFKWDYDLV 299  
DB 241 LAKNLVANKECEFKRIVAINVVKWNTLMHLDLWTLMDKNKFLYSPIANVDFKWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASTINKEPVLIPGGAGATEMETARETNDGTNYIAIKPGL 359  
DB 301 NGGAEPQPVNGLPLEKLLQSLINKKPVLIPTAGAGASQMEITERTHFDGTNYIAIRPGV 360  
QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRDKVK 408  
DB 361 VIGYDRNEKTNALKAAGIKVLPPHGNQLSLGMGNARCMSPLSRDKVK 409  
RESULT 14  
ADP79616  
ID ADP79616 standard; protein; 409 AA.  
XX  
AC ADP79616;  
XX

DT 04-NOV-2004 (first entry)  
XX Mycoplasma arthritis arginine deaminase variant.  
DE  
XX Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
XX Mycoplasma arthritis.  
OS  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 112  
FT /label= K112E  
FT /note= "wild-type Lys is substituted with with Glu"  
XX  
XX WO2004046309-A2.  
PN  
XX  
PD 03-JUN-2004.  
XX  
XX 29-SEP-2003; 2003WO-US030770.  
PF  
XX  
XX 18-NOV-2002; 2002US-0427497P.  
PR  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
PA  
XX Clark MA;  
PI WPI; 2004-431965/40.  
XX  
XX Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
XX Claim 18; SEQ ID NO 10; 89pp; English.  
XX  
XX The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma arthritis arginine deaminase variant.  
XX  
XX Sequence 409 AA;  
Query Match 84.6%; Score 1793.5; DB 8; Length 409;  
Best Local Similarity 84.1%; Pred. No. 2.4e-162; Mismatches 34; Indels 1; Gaps 1;  
Matches 344; Conservative 30;  
QY 1 MSVFDKFGNHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
DB 1 MSVFDKFGNHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
QY 61 FVKMKRGINVELTDLVAETDYDLASAKAEETFTLEETVPLTANKKAVRAFLLS 120  
DB 61 FVAILKANDINNVETIDLVAETDYDLASQAEKDRLEEFLEDEPVLSEAHKVVNFLLKA 120  
QY 121 KPT-HEMVDFWMSGITKYELGVSENELIVDPMNLYETRDPPFASVGVNGVTIHFMYIVR 179  
DB 121 KKTSRKLVLMWAGITKYDVGAEADHELIYDPMNLYETRDPPFASVGVNGVTIHFMYIVR 180  
QY 180 RRETLFARFVFNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239  
DB 181 RRETLFARFVFNHPKLVNTWYDPAKMLSTEGGDVFIYNNETLVVGVSERTDLDITL 240  
QY 240 LAKNIKANKEVEFKRIVAINVVKWNTLMHLDLWTLMDKNKFLYSPIANVDFKWDYDLV 299

Db 241 LAKNLVANKECFKRIIVAINVVKWNTLMHLDIWLTLMDKNKFLYSPIANDVFKWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIRPGL 359  
Db 301 NGGAEPQVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYTAIRPGV 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQSLGGMGNARCMSPLSRDKVK 408  
Db 361 VIGYSRNEKTNAAALKAAGIKVLPFHGNQSLGGMGNARCMSPLSRDKVK 409

RESULT 15  
ADP79615  
ID ADP79615 standard; protein; 409 AA.  
XX  
AC ADP79615;  
DT 04-NOV-2004 (first entry)  
XX  
DE Mycoplasma arthritidis arginine deaminase variant.  
XX  
KW Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
OS Mycoplasma arthritidis.

FH Key Location/Qualifiers  
FT Misc-difference 111 /label= K111E  
FT /note= "wild-type Lys is substituted with with Glu"  
XX  
XX WO2004046309-A2.  
XX  
PD 03-JUN-2004.  
XX  
XX 29-SEP-2003; 2003WO-US030770.  
XX  
XX 18-NOV-2002; 2002US-0427497P.  
XX  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
XX Clark MA;  
XX  
XX WPI; 2004-431965/40.  
XX  
XX Inhibiting replication of viruses in individual, involves administering  
XX composition comprising arginine deaminase bonded to polyethylene glycol,  
XX to individual.  
XX  
XX Claim 18; SEQ ID NO 9; 89pp; English.

XX The invention relates to inhibiting the replication of one or more  
XX viruses in an individual and involves administering to the individual a  
XX composition comprising an arginine deaminase bonded to polyethylene  
XX glycol. The method is useful for inhibiting replication of one or more  
XX viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
XX where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
XX M. hominis, M. arthritidis and its combination. It is useful for treating  
XX an individual who is suspected of having been exposed to one or more  
XX viruses, for modulating nitric oxide levels in an individual, or for  
XX selectively inhibiting viral replication in an individual. The method is  
XX also useful for treating a tumour and inhibiting replication of one ore  
XX more viruses in an individual. The tumour is melanoma, sarcoma, or  
XX hepatoma. The tumour is hepatocellular carcinoma. The method is also  
XX useful for improving liver function in an individual. The present  
XX sequence represents a Mycoplasma arthritidis arginine deaminase variant.

XX Sequence 409 AA;  
Query Match 84.6%; Score 1793.5; DB 8; Length 409;  
Best Local Similarity 84.1%; Pred. No. 2.4e-162;  
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDKFNHGVHYSEIGELETVLVHEPGRREIDYITPARDELIFSAILESHDARKEHQ 60  
Db 1 MSVFDKFKGIHYVSEIGELESVLVHEPGRREIDYITPARDELIFSAILESHDARKEQSQ 60  
QY 61 FVKIMKDRGINNVELTDLVAETVDLASKAAKBEPIETFBETVPVLTEANKKAVRAFLLS 120  
Db 61 FVALKANDINNVETIDLVAETVDLASEAKDRLIBEFLEDESEPVLSAHEKVVVRNFKA 120  
QY 121 KPT-HEMVFEFMSGITKYVELGVSENELIVDPENLYFTRDPFASVGVGVTHIHEMRYIVR 179  
Db 121 KKTSRKLVELMMAGITKYDLGVEADHELI VDPENLYFTRDPFASVGVGVTHIHEMRYIVR 180  
QY 180 RRETLFARFVRNHPKLVKTPWYYDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITTL 239  
Db 181 RRETLSRFRVRNHPKLVNTPTWYYDPAMKLSIEGGDVFIYNNDLTVVGVSERTDLDITVL 240  
QY 240 LAKNIVANKEVEFKRIIVAINVVKWNTLMHLDIWLTLMDKNKFLYSPIANDVFKWDYDLV 299  
Db 241 LAKNLVANKECFKRIIVAINVVKWNTLMHLDIWLTLMDKNKFLYSPIANDVFKWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIRPGL 359  
Db 301 NGGAEPQVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYTAIRPGV 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQSLGGMGNARCMSPLSRDKVK 408  
Db 361 VIGYSRNEKTNAAALKAAGIKVLPFHGNQSLGGMGNARCMSPLSRDKVK 409

Search completed: April 6, 2005, 06:30:19  
Job time : 177 secs

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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:04 ; Search time 24 Seconds  
(without alignments)  
1272.144 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVFDSEKNGIHVYSEIGEL.....LGMGNARCMPLSRKDVKW 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	100.0	409	3	US-09-023-809B-3
2	2120	100.0	409	4	US-09-564-559B-1
3	2120	100.0	409	4	US-09-723-546-3
4	2116	99.8	409	4	US-09-564-559B-2
5	2112	99.6	409	4	US-09-564-559B-3
6	2108	99.4	409	4	US-09-564-559B-4
7	2098.5	98.0	410	1	US-08-792-283A-8
8	2098.5	99.0	410	2	US-09-105-908-8
9	2098.5	99.0	410	3	US-09-271-713-8
10	1807.5	85.3	410	3	US-09-023-809B-2
11	1807.5	85.3	410	4	US-09-723-546-2
12	1793.5	84.6	409	4	US-09-564-559B-7
13	1789.5	84.4	409	4	US-09-564-559B-9
14	1789.5	84.4	409	4	US-09-564-559B-10
15	1785.5	84.2	409	4	US-09-564-559B-8
16	1765.5	83.3	410	1	US-08-792-283A-7
17	1765.5	83.3	410	2	US-09-105-908-7
18	1765.5	83.3	410	3	US-09-271-713-7
19	1764.5	83.2	410	3	US-09-023-809B-1
20	1764.5	83.2	410	4	US-09-723-546-1
21	1746.5	82.4	409	4	US-09-564-559B-5
22	1742.5	82.2	409	4	US-09-564-559B-6
23	1732.5	81.7	410	1	US-08-792-283A-2
24	1732.5	81.7	410	2	US-09-105-908-2
25	1732.5	81.7	410	3	US-09-271-713-2
26	1713.5	80.8	410	1	US-08-792-283A-9
27	1713.5	80.8	410	2	US-09-105-908-9

28	1713.5	80.8	410	3	US-09-271-713-9
29	1698.5	80.1	399	6	5474928-2
30	1698.5	80.1	399	6	5474928-2
31	681.5	32.1	413	4	US-09-723-546-12
32	679	32.0	411	4	US-09-723-546-6
33	670.5	31.6	408	4	US-09-723-546-13
34	667.5	31.5	417	4	US-09-107-532A-6148
35	655	30.9	413	4	US-09-723-546-11
36	652.5	30.8	409	4	US-09-583-110-4274
37	652.5	30.8	413	4	US-09-107-433-3204
38	651.5	30.7	409	4	US-09-723-546-7
39	640.5	30.2	411	3	US-08-964-652-2
40	640.5	30.2	422	3	US-09-134-001C-2931
41	625	29.5	409	4	US-09-723-546-14
42	618	29.2	420	3	US-09-134-001C-4427
43	612.5	28.9	410	4	US-09-723-546-8
44	604.5	28.5	394	4	US-09-710-279-58
45	600.5	28.3	409	4	US-09-723-546-9

ALIGNMENTS

RESULT 1

US-09-023-809B-3  
; Sequence 3, Application US/09023809B  
; Patent No. 6183738  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A  
; TITLE OF INVENTION: Modified Arginine Deiminase  
; FILE REFERENCE: PH00028  
; CURRENT APPLICATION NUMBER: US/09/023,809B  
; CURRENT FILING DATE: 2000-02-13  
; PRIOR APPLICATION NUMBER: 60/046,200  
; PRIOR FILING DATE: 1997-05-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-09-023-809B-3

Query Match	100.0%	Score	2120;	DB	3;	Length	409;
Best Local Similarity	100.0%	Pred. No.	2e-212;				
Matches	409;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MSVFDSEKNGIHVYSEIGEL	TVLVHVEPGREIDYITPARLDEL	LSFALES	HDARKEHQ	60	
Db	1	MSVFDSEKNGIHVYSEIGEL	TVLVHVEPGREIDYITPARLDEL	LSFALES	HDARKEHQ	60	
Qy	61	FKIMKDRGINVVELTDLVAET	YDLASAKAAKEEFLETETPVL	TEANKKAVRAFL	LLS	120	
Db	61	FKIMKDRGINVVELTDLVAET	YDLASAKAAKEEFLETETPVL	TEANKKAVRAFL	LLS	120	
Qy	121	KPTHEMVEFMMSGITKYELG	VESENELIVDPMPNLVYFRDPP	PASVGVNGVTIHFMYIVR	180		
Db	121	KPTHEMVEFMMSGITKYELG	VESENELIVDPMPNLVYFRDPP	PASVGVNGVTIHFMYIVR	180		
Qy	181	RETLFARVFRNHPKLVKTPY	YDPAMKPIEGGDVFIYNNETL	VGVYSERTDLOTITLL	240		
Db	181	RETLFARVFRNHPKLVKTPY	YDPAMKPIEGGDVFIYNNETL	VGVYSERTDLOTITLL	240		
Qy	241	AKNIKANKEVEFKRIVA	INVPKWTNMLDITWLTKNKNK	FLYSPIANDVFKFWDV	DLVN	300	
Db	241	AKNIKANKEVEFKRIVA	INVPKWTNMLDITWLTKNKNK	FLYSPIANDVFKFWDV	DLVN	300	
Qy	301	CGAEFPQQLGPLDKLLAS	IINKEPVLIPIGGAGATEMEI	ARETNFDCGTNYLAIKPGL	360		
Db	301	CGAEFPQQLGPLDKLLAS	IINKEPVLIPIGGAGATEMEI	ARETNFDCGTNYLAIKPGL	360		
Qy	361	IGYDRNEKTNAAKAGITV	LPFHGNQISLGNARCMPLSR	KDVKW	409		
Db	361	IGYDRNEKTNAAKAGITV	LPFHGNQISLGNARCMPLSR	KDVKW	409		

Db 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 2

US-09-564-559B-1

; Sequence 1, Application US/09564559B

; Patent No. 6635462

; GENERAL INFORMATION:

; APPLICANT: Ensor, Charles Mark

; APPLICANT: Holtsberg, Frederick Wayne

; APPLICANT: Clark, Mike A.

; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase

; FILE REFERENCE: PHOE0033

; CURRENT APPLICATION NUMBER: US/09/564,559B

; CURRENT FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: 09/564,559

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: PCT/US01/14116

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 409

; TYPE: PRT

; ORGANISM: Mycoplasma hominis

US-09-564-559B-1

Query Match 100.0%; Score 2120; DB 4; Length 409;

Best Local Similarity 100.0%; Pred. No. 2e-212;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKFNHGVSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60

DB 1 MSVFDKFNHGVSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60

QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFL 120

DB 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFL 120

QY 121 KPTHEWVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGVNGVTIHFMYIYVR 180

DB 121 KPTHEWVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGVNGVTIHFMYIYVR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240

DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240

QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVPKFWDYDLVN 300

DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVPKFWDYDLVN 300

QY 301 GGAEPQOLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360

DB 301 GGAEPQOLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360

QY 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

DB 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 3

US-09-723-546-3

; Sequence 3, Application US/09723546

; Patent No. 6737259

; GENERAL INFORMATION:

; APPLICANT: Clark, Mike A

; APPLICANT: Modified Arginine Deiminase

; FILE REFERENCE: PHOE0059

; CURRENT APPLICATION NUMBER: US/09/723,546

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 09/023,809

; PRIOR FILING DATE: 1998-02-13

; NUMBER OF SEQ ID NOS: 14

Query Match 99.8%; Score 2116; DB 4; Length 409;

Best Local Similarity 99.8%; Pred. No. 5.3e-212;

Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKFNHGVSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60

DB 1 MSVFDKFNHGVSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60

QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFL 120

DB 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFL 120

QY 121 KPTHEWVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGVNGVTIHFMYIYVR 180

DB 121 KPTHEWVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGVNGVTIHFMYIYVR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240

DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITLL 240

QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVPKFWDYDLVN 300

DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVPKFWDYDLVN 300

QY 301 GGAEPQOLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360

DB 301 GGAEPQOLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360

QY 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

DB 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409



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Db 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120
Qy 121 KPTHEWVFMSGITHVYSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 60
Db 121 KPTHEWVFMSGITHVYSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 60
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITILL 240
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITILL 240
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVKFWDYDLVN 300
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVKFWDYDLVN 300
Qy 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Db 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNAALKAAGITVLPFFHGNQLSLGNGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKTNAALKAAGITVLPFFHGNQLSLGNGNARCMSPLSRKDVKW 409

RESULT 5
US-09-564-559B-3
; Sequence 3, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-3

Query Match 99.6%; Score 2112; DB 4; Length 409;
Best Local Similarity 99.8%; Pred. No. 1.4e-211;
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSVFDKFNHGVSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 60
Db 1 MSVFDKFNHGVSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120
Db 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120
Qy 121 KPTHEWVFMSGITHVYSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 180
Db 121 KPTHEWVFMSGITHVYSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 180
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITILL 240
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITILL 240
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVKFWDYDLVN 300
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVKFWDYDLVN 300
Qy 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Db 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
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Db 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNAALKAAGITVLPFFHGNQLSLGNGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKTNAALKAAGITVLPFFHGNQLSLGNGNARCMSPLSRKDVKW 409

RESULT 6
US-09-564-559B-4
; Sequence 4, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-4

Query Match 99.4%; Score 2108; DB 4; Length 409;
Best Local Similarity 99.5%; Pred. No. 3.6e-211;
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSVFDKFNHGVSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 60
Db 1 MSVFDKFNHGVSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120
Db 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120
Qy 121 KPTHEWVFMSGITHVYSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 180
Db 121 KPTHEWVFMSGITHVYSEIGLETVLVHPEGRIDYITPARLDELLFSAILESHDARKEHQ 180
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITILL 240
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSERTDLDITILL 240
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVKFWDYDLVN 300
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVKFWDYDLVN 300
Qy 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Db 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNAALKAAGITVLPFFHGNQLSLGNGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKTNAALKAAGITVLPFFHGNQLSLGNGNARCMSPLSRKDVKW 409

RESULT 7
US-08-792-283A-8
; Sequence 8, Application US/08792283A
; Patent No. 5804183
; GENERAL INFORMATION:
; APPLICANT: Filpula, David
; APPLICANT: Wang, Maoliang
; TITLE OF INVENTION: Arginine Deiminase Derived From
```

;; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ROBERTS & MERCANTI  
;; STREET: 81 Tamarack Circle  
;; CITY: Skillman  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 08558  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/792,283A  
;; FILING DATE: 31-JAN-1997  
;; CLASSIFICATION: 428  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mercanti, Michael N.  
;; REGISTRATION NUMBER: 33966  
;; REFERENCE/DOCKET NUMBER: 2131055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-921-3500  
;; TELEFAX: 609-921-9535  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 410 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycoplasma hominis  
;; STRAIN: PG21  
;; CELL TYPE: unicellular  
US-08-792-283A-8

Query Match 99.0%; Score 2098.5; DB 1; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.6e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 MSVFDKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFPALLESHDARKEHQ 60  
DB |||||  
QY 1 MSVFDKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFPALLESHDARKEHQ 60  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLETETLTPVLTANKKAVRAFLLS 120  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLETETLTPVLTANKKAVRAFLLS 120  
DB |||||  
QY 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMYIVR 179  
DB |||||  
QY 121 QKPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMYIVR 180  
DB |||||  
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVGVGSRTDLDTITL 239  
DB |||||  
QY 181 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVGVGSRTDLDTITL 240  
DB |||||  
QY 240 LAKNIKANKEVEFKRIVAINVPAKTNLMHLDITLMDKNKFLYSPANDVFKFWDYDLV 299  
DB |||||  
QY 241 LAKNIKANKEVEFKRIVAINVPAKTNLMHLDITLMDKNKFLYSPANDVFKFWDYDLV 300  
DB |||||  
QY 300 NGGAPQPOLNGLPLDKLLASINKEPVLIPGGAGATEMEIARETNPDGNTYLAIRKPL 359  
DB |||||  
QY 301 NGGAPQPOLNGLPLDKLLASINKEPVLIPGGAGATEMEIARETNPDGNTYLAIRKPL 360  
DB |||||  
QY 360 VIGYDRNEKTNALKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVK 409  
DB |||||  
QY 361 VIGYDRNEKTNALKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVK 410  
DB |||||

RESULT 8

US-09-105-908-8  
;; Sequence 8, Application US/09105908  
;; Patent No. 5916793  
;; GENERAL INFORMATION:  
;; APPLICANT: Filpula, David  
;; APPLICANT: Wang, Maoliang  
;; TITLE OF INVENTION: Arginine Deiminase Derived From  
;; MYCOPLASMA AND POLYMER CONJUGATES CONTAINING THE SAME  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ROBERTS & MERCANTI  
;; STREET: 81 Tamarack Circle  
;; CITY: Skillman  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 08558  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/105,908  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: US/08/792,283  
;; FILING DATE: 31-JAN-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mercanti, Michael N.  
;; REGISTRATION NUMBER: 33966  
;; REFERENCE/DOCKET NUMBER: 2131055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-921-3500  
;; TELEFAX: 609-921-9535  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 410 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: No. 5916793 Relevant  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycoplasma hominis  
;; STRAIN: PG21  
;; CELL TYPE: unicellular  
US-09-105-908-8

Query Match 99.0%; Score 2098.5; DB 2; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.6e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 MSVFDKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFPALLESHDARKEHQ 60  
DB |||||  
QY 1 MSVFDKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFPALLESHDARKEHQ 60  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLETETLTPVLTANKKAVRAFLLS 120  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFLETETLTPVLTANKKAVRAFLLS 120  
DB |||||  
QY 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMYIVR 179  
DB |||||  
QY 121 QKPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMYIVR 180  
DB |||||  
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVGVGSRTDLDTITL 239  
DB |||||  
QY 181 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVGVGSRTDLDTITL 240  
DB |||||  
QY 240 LAKNIKANKEVEFKRIVAINVPAKTNLMHLDITLMDKNKFLYSPANDVFKFWDYDLV 299  
DB |||||  
QY 241 LAKNIKANKEVEFKRIVAINVPAKTNLMHLDITLMDKNKFLYSPANDVFKFWDYDLV 300  
DB |||||

QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTNYLAIKPGL 359  
Db 301 NGGAEPQVPLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTNYLAIKPGL 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMWPLSRKDVW 409  
Db 361 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMWPLSRKDVW 410

RESULT 9  
US-09-271-713-8  
; Sequence 8, Application US/09271713  
; Patent No. 6132713  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David  
; APPLICANT: Wang, Maoliang  
; TITLE OF INVENTION: Arginine Deiminase Derived From  
; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBERTS & MERCANTI  
; STREET: 81 Tamarack Circle  
; CITY: Skillman  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 08558  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/271,713  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/792,283  
; FILING DATE: 31-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mercanti, Michael N.  
; REGISTRATION NUMBER: 33966  
; REFERENCE/DOCKET NUMBER: 2131055  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-921-3500  
; TELEFAX: 609-921-9535  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 410 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. 6132713 Relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mycoplasma hominis  
; STRAIN: PG21  
; CELL TYPE: unicellular  
US-09-271-713-8

Query Match 99.0%; Score 2098.5; DB 3; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.6e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MSVDSKFNGLHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
Db 1 MSVDSKFNGLHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLS 120  
QY 121 -KPTHEMVFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 179

Db 121 QKPTHEMVFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 180  
QY 180 RRETLLFARFVRNHPKLVKTPWYVDPAMKMPIEGGDVFIYNNETLVVGVSRDTLDTITL 239  
Db 181 RRETLLFARFVRNHPKLVKTPWYVDPAMKMPIEGGDVFIYNNETLVVGVSRDTLDTITL 240  
QY 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDLTWLTMDKNKFLYSPIANDPKFWDYDLV 299  
Db 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDLTWLTMDKNKFLYSPIANDPKFWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTNYLAIKPGL 359  
Db 301 NGGAEPQVPLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTNYLAIKPGL 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMWPLSRKDVW 409  
Db 361 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMWPLSRKDVW 410

RESULT 10  
US-09-023-809B-2  
; Sequence 2, Application US/09023809B  
; Patent No. 6183738  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A  
; TITLE OF INVENTION: Modified Arginine Deiminase  
; FILE REFERENCE: PHOE0028  
; CURRENT APPLICATION NUMBER: US/09/023,809B  
; CURRENT FILING DATE: 2000-02-13  
; PRIOR APPLICATION NUMBER: 60/046,200  
; PRIOR FILING DATE: 1997-05-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 410  
; TYPE: PPT  
; ORGANISM: Mycoplasma arthritidis  
US-09-023-809B-2

Query Match 85.3%; Score 1807.5; DB 3; Length 410;  
Best Local Similarity 84.4%; Pred. No. 8.6e-180;  
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVDSKFNGLHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
Db 1 MSVDSKFNGLHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLS 120  
QY 121 KPT-HEMVFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 179  
Db 121 KTSRKLVELMAGITKYDLGVADHLLIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 180  
QY 180 RRETLLFARFVRNHPKLVKTPWYVDPAMKMPIEGGDVFIYNNETLVVGVSRDTLDTITL 239  
Db 181 RRETLLFARFVRNHPKLVKTPWYVDPAMKMPIEGGDVFIYNNETLVVGVSRDTLDTITL 240  
QY 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDLTWLTMDKNKFLYSPIANDPKFWDYDLV 299  
Db 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDLTWLTMDKNKFLYSPIANDPKFWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTNYLAIKPGL 359  
Db 301 NGGAEPQVPLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTNYLAIRPGV 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMWPLSRKDVW 409  
Db 361 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMWPLSRKDVW 410

RESULT 11

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US-09-723-546-2
; Sequence 2, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-723-546-2

Query Match      85.3%; Score 1807.5; DB 4; Length 410;
Best Local Similarity 84.4%; Pred. No. 8.6e-180;
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 60
Db 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELFLSAILSHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 120
Db 61 FVAILKANDINVETIDLVAEYDYLASQAKRKIEEFLEDESEFVLSAHHKKVVRNFLKA 120
Qy 121 KPT-HEMVFEFMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGVNGVTIHFMRIVYR 179
Db 121 KKTSRKLVELMMAGITKYDLGVADHLLIVDPMNLYFTTRDPFASVGVNGVTIHFMRIVYR 180
Qy 180 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDITL 239
Db 181 RRETLPFRFVRNHPKLVNTPWYDPAKMLSIGGDVFIYNNETLVVGVSERTDITL 240
Qy 240 LAKNIKANKVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDFKWDYDLV 299
Db 241 LAKNLVANKECFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDFKWDYDLV 300
Qy 300 NGGAEPQPLNGPLDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTYNLAIKPGL 359
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGSGASQMEIERETHFDGTYNLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409
Db 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQSLGNGNARCMSPLSRKDVK 409

RESULT 12
US-09-564-559B-7
; Sequence 7, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-7

Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 60
Db 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELFLSAILSHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 120
Db 61 FVAILKANDINVETIDLVAEYDYLASQAKRKIEEFLEDESEFVLSAHHKKVVRNFLKA 120
Qy 121 KPT-HEMVFEFMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGVNGVTIHFMRIVYR 179
; TYPE: PRT
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; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-7

Query Match      84.6%; Score 1793.5; DB 4; Length 409;
Best Local Similarity 84.4%; Pred. No. 2.5e-178;
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 60
Db 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELFLSAILSHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 120
Db 61 FVAILKANDINVETIDLVAEYDYLASQAKRKIEEFLEDESEFVLSAHHKKVVRNFLKA 120
Qy 121 KPT-HEMVFEFMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGVNGVTIHFMRIVYR 179
Db 121 KKTSRKLVELMMAGITKYDLGVADHLLIVDPMNLYFTTRDPFASVGVNGVTIHFMRIVYR 180
Qy 180 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDITL 239
Db 181 RRETLPFRFVRNHPKLVNTPWYDPAKMLSIGGDVFIYNNETLVVGVSERTDITL 240
Qy 240 LAKNIKANKVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDFKWDYDLV 299
Db 241 LAKNLVANKECFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDFKWDYDLV 300
Qy 300 NGGAEPQPLNGPLDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTYNLAIKPGL 359
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGSGASQMEIERETHFDGTYNLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQSLGNGNARCMSPLSRKDVK 409

RESULT 13
US-09-564-559B-9
; Sequence 9, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-9

Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 60
Db 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELFLSAILSHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLALASKAAKEEFIEFTFLEETVPLTEANKKAVRAFLLS 120
Db 61 FVAILKANDINVETIDLVAEYDYLASQAKRKIEEFLEDESEFVLSAHHKKVVRNFLKA 120
Qy 121 KPT-HEMVFEFMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGVNGVTIHFMRIVYR 179
; TYPE: PRT
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Db 121 KTSRKLVELMMAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVGVTTHFMYKVR 180
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Db 181 RRETILFSRFRNHPKLVNTWPYDPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAEPQPOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGNTYLAIKPGL 359
Db 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPAGEGASQMEIERETHFDGNTYIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGNGNARCMSPLSRKDVK 409

RESULT 14
US-09-564-559B-10
; Sequence 10, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-10

Query Match 84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKFGIHVYSEIGELETVLVHEPGREIDYITPARLDELFLSAILSHDARKEHQ 60
Db 1 MSVFDSEKFGIHVYSEIGELESVLVHEPGREIDYITPARLDELFLSAILSHDARKEHQ 60
QY 61 FVKIMKDRGINVELTDLVAETDYDLASAKAEETETETETETETETETETETETETET 120
Db 61 FVAILKANDINVTETDLVAETDYDLASQAKDKIEEFLEDESEPLSEAHKEVVRNFLKA 120
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVGVTTHFMYKVR 179
Db 121 KTSRKLVELMMAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVGVTTHFMYKVR 180
QY 180 RRETILFARFVRNHPKLVKTPWYDPAMKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETILFSRFRNHPKLVNTWPYDPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAEPQPOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGNTYLAIKPGL 359
Db 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPAGEGASQMEIERETHFDGNTYIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGNGNARCMSPLSRKDVK 409

Search completed: April 6, 2005, 06:27:18
Job time : 26 secs
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Db 121 KTSRKLVELMMAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVGVTTHFMYKVR 180
QY 180 RRETILFARFVRNHPKLVKTPWYDPAMKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETILFSRFRNHPKLVNTWPYDPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAEPQPOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGNTYLAIKPGL 359
Db 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPAGEGASQMEIERETHFDGNTYIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGNGNARCMSPLSRKDVK 409

RESULT 14
US-09-564-559B-10
; Sequence 10, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-10

Query Match 84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKFGIHVYSEIGELETVLVHEPGREIDYITPARLDELFLSAILSHDARKEHQ 60
Db 1 MSVFDSEKFGIHVYSEIGELESVLVHEPGREIDYITPARLDELFLSAILSHDARKEHQ 60
QY 61 FVKIMKDRGINVELTDLVAETDYDLASAKAEETETETETETETETETETETETETET 120
Db 61 FVAILKANDINVTETDLVAETDYDLASQAKDKIEEFLEDESEPLSEAHKEVVRNFLKA 120
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVGVTTHFMYKVR 179
Db 121 KTSRKLVELMMAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVGVTTHFMYKVR 180
QY 180 RRETILFARFVRNHPKLVKTPWYDPAMKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETILFSRFRNHPKLVNTWPYDPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAEPQPOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGNTYLAIKPGL 359
Db 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPAGEGASQMEIERETHFDGNTYIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVK 408
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